

Figure 1: 254P1D6B SSH sequence of 186 nucleotides (SEQ ID NO: 1).

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1  GATCCACAGA TAGGACACAA TTCTTTGGTC ATCAGTAGAC CTTGAACCAT CCAAAGTAAT
61  GGAATTATTG GGAAGCACAA GAACATGTCT GCCACCAGCC CGGGCTCTGG GAGGACTATT
121 ATTTTCCTTC TTCACAGCCA CAGTGAGGGT GGACGTGCTG CTCAGTCCCT GCTGGTCTTT
181 TACTGTCAAA CGGAAGTGGT AGGTCCCCAC CTGGAGACCA GTCACAGTGG CTATTGCTTT
241 GTCAATATTT TCCATCTCCA CTGCACTGGG GCCTCTGACG TGCT
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Figure 2:

1 gctgcgcggcgccggtgggtggggatcccccggggggtgcacactttgctccacccttgctgtgc
61 cctcggcgccggccttgggtgagccccgcgcagagcgggcgggcgctcgtgtcactggccgga
121 ggtagagagcgcagcagtagatttcagccctgtccttggggcttgggtccagattcgcctcctctgg
181 ggctacgtccccggggaaagaggaaagcgaggyatttttgcgtgggggtgggggtgttacctcttaac
241 agcaggtgcgcgcgcgaggggtgtgaacctgtgtgttgtgtgtgtgtstgtgtgtgtgtgtgtgt
301 taagacctgcgatgaacgacgaggayaggaacaagtggggacgycgagtgatgctcagggccag
361 cagcaacgcctatggggcgagcttcagtgtcgccagcagtgaccacagttctttagggccaaa
421 tctggctcctaasaaaaacatcaaagggaagccttgacccaaaactctcttcaggggccgcctcag
1 M A P P T G V L S S
481 aagcctgcccatcaccccactgtgtgggtgcacaATGGCGCCCCCCCACAGGTGTCCTCTCTTC
11 L L L L V T I A G C A R K Q C S E G R T
541 ATTGCTGCTGCTGGTGACAATTGCAGGTTGTGCCCGTAAGCAGTGCAGCGAGGGGAGGAC
31 Y S N A V I S P N L E T T R I M R V S H
601 ATATTCCAATGCAGTCAATTCACCTAACTTGGAACCACCAGAATCATGCGGGTGTCTCA
51 T F P V V D C T A A C C D L S S C D L A
661 CACCTTCCCTGTGCTAGACTGCACGGCCGCTTGCTGTGACCTGTCCAGCTGTGACCTGGC
71 W W F E G R C Y L V S C P H K E N C E P
721 CTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCCCCACAAAGAGAACTGTGAGCC
91 K K M G P I R S Y L T F V L R F V Q R P
781 CAAGAAGATGGCCCCCATCAGGTCTTATCTCACTTTTGTGCTCCGGCCTGTTTCAGAGGCC
111 A Q L L D Y G D M M L N R G S P S G I W
841 TGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGSGGCTCCCCCTCGGGGATCTG
131 G D S P E D I R K D L P F L G K D W G L
901 GGGGGACTCACTGAGGATATCAGAAAAGGACTTGMCCCTTTCTAGGCAAAGATTGGGGCCT
151 E E M S E Y S D D Y R E L E K D L L Q P
961 AGAGGAGATGTCTFGAGTACKCAGATGACTACCGGGAGCTGGAGAAGGACCTCTTGCAACC
171 S G K Q E P R G S A E Y T D W G L L P G
1021 CAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACGGACTGGGGCCTACTGCCGGG
191 S E G A F N S S V G D S P A V P A E T Q
1081 CAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCCTGCGGTGCCAGCGGAGACGCA
211 Q D F E L H Y L N E S A S T P A P K L P
1141 GCAGGACCCCTGAGCTCCATTACCTGAATGAGTCGGCTTCAACCCCTGCCCCAAAACCTCCC
231 E R S V L L P L P T T P S S G E V L E K
1201 TGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCTTCAGGAGAGGTGTTGGAGAA
251 E K A S Q L Q E Q S S N S S G K E V L M
1261 AGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGCTCTGGAAAAGAGGTTCTAAT
271 P S H S L P P A S L E L S S V T V E K S

Figure 2A-2

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1321 GCCTFCCCATAGTCTTCCTCCGGCAAGCCTGGAGCTCAGCTCAGTCACCGTGGAGAAAAG
291 P V L T V T P G S T E H S I P T P P T S
1381 CCCAGTGGCTCACAGTCACCCCGGGGAGTACAGAGCACAGCATCCCAACACCTCCCACTAG
311 A A P S E S T P S E L P T S P T T A P R
1441 CGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATATCTCCTACCACTGCTCCCAG
331 T V K E L T V S A G D N L I I T L P D N
1501 GACAGTGAAAGAACTTACGGTATCGGCTGGAGATAACCTAATTATAACTTTACCCGACAA
351 E V E L K A F V A P A P P V E T T Y N Y
1561 TGAAGTTGAACTGAAGGCCTTTGTTGCGCCAGCGCCACCTGTAGAAACAACCTACAACCTA
371 E W N L I S H P T D Y Q G E I K Q G H K
1621 TGAATGGAATTTAATAAGCCACCCACAGACTACCAAGGTGAAATAAAACAAGGACACAA
391 Q T L N L S Q L S V G L Y V F K V T V S
1681 GCAAACCTCTTAACCTCTCTCAATTGTCCGTCGGACTTTATGTCTTCAAAGTCACTGTTTC
411 S E N A F G E G F V N V T V K P A R R V
1741 TAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCACTGTTAAGCCTGCCAGAAGAGT
431 N L P P V A V V S P Q L Q E L T L P L T
1801 CAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAAGAGCTCACTTTGCCTTTGAC
451 S A L I D G S Q S T D D T E I V S Y H W
1861 GTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACTGAAATAGTGAGTTATCATTG
471 E E I N G P F I E E K T S V D S P V L R
1921 GGAAGAAATAAACGGGCCCTTCATAGAAGAGAAGACTTCAGTTGACTCTCCCGTCTTACG
491 L S N L D P G N Y S F R L T V T D S D G
1981 CTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTGACTGTTACAGACTCGGACGG
511 A T N S T T A A L I V N N A V D Y P P V
2041 AGCCACTAACTCTACAACCTGCAGCCCTAATAGTGAACAATGCTGTGGACTACCCACCAGT
531 A N A G P N H T I T L P Q N S I T L N G
2101 TGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAAAACCTCCATCACTTTGAATGG
551 N Q S S D D H Q I V L Y E W S L G P G S
2161 AAACCAGAGCAGTGACGATCACCAGATTGTCTCTATGAGTGGTCCCTGGGTCTCTGGGAG
571 E G K H V V M Q G V Q T P Y L H L S A M
2221 TGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCATACCTTCATTTATCTGCAAT
591 Q E G D Y F F Q L K V T D S S R Q Q S T
2281 GCAGGAAGGAGATTATACATTTAGCTGAAGGTGACAGATTCTTCAAGGCAACAGTCTAC
611 A V V T V I V Q P E N N R P P V A V A G
2341 TGCTGTRGTGACTGTGATTGTCCAGCCTGAAAACAATAGACCTCCAGTGGCTGTGGCCGG
631 P D K E L I F P V E S A T L D G S S S S
2401 CCCTGATAAAGAGCTGATCTTCCAGTGGAAAGTGCTACCCCTGGATGGGAGCAGCAGCAG
651 D D H G I V F Y H W E H V R G P S A V E
2461 CGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTGAGAGGCCCACTGTCAGTGGGA
671 M E N I D K A I A T V T G L Q V G T Y H
2521 GATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGTCTCCAGGTGGGGACCTACCA

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Figure 2A-3

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691 F R L T V K D Q Q G L S S T S T L T V A
2581 CTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGCACGTCCACCCTCACTGTGGC
711 V K K E N N S P P R A R A G G R H V L V
2641 TGTGAAGAAGGAAAATAATAGTCCTCCAGAGCCCCGGGCTGGTGGCAGACATGTTCTTGT
731 L P N N S I T L D G S R S T D D Q R I V
2701 GCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCTACTGATGACCAAAGAATTGT
751 S Y L W I R D G Q S P A A G D V I D G S
2761 GTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCTGGAGATGTCATCGATGGCTC
771 D H S V A L Q L T N L V E G V Y T F H L
2821 TGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAGGGGGTGTACACTTTCACCTT
791 R V T D S Q G A S D T D T A T V E V Q P
2881 GCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACTGCCACTGTGGAAGTGCAGCC
811 D P R K S G L V E L T L Q V G V G Q L T
2941 AGACCCTAGGAAGAGTGGCCTGCTGGAGCTGACCTGCAGGTTGGTGTGGGCAGCTGAC
831 E Q R K D T L V R Q L A V L L N V L D S
3001 AGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTGCTGCTGAACGTGCTGGACTC
351 D I K V Q K I R A H S D L S T V I V F Y
3061 GGACATTAAGGTCCAGAAGATTGGGGCCCACTCGGATCTCAGCACCGTGATTGTGTTTTA
871 V Q S R P P F K V L K A A E V A R N L H
3121 TGTACAGAGCAGGCCCGCCTTTCAAGGTTCTCAAAGCTGCTGAAGTGGCCCCGAAATCTGCA
891 M R L S K E K A D F L L F K V L R V D T
3181 CATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTCAAGGTCTTGAGGGTTGATAC
911 A G C L L K C S G H G H C D P L T K R C
3241 AGCAGGTTGCCTTCTGAAGTGTCTGGCCATGGTCACTGCGACCCCTCACAAAGCGCTG
931 I C S H L W M E N L I Q R Y I W D G E S
3301 CATTTGCTCTCACTTATGGATGGAGAACCCTTATACAGCCTTATATCTGGGATGGAGAGAG
951 N C E W S I F Y V T V L A F T L I V L T
3361 CAACTGTGAGTGGAGTATATTCTATGTGACAGTGTGGCTTTTACTCTTATTGTGCTAAC
971 G G F T W L C I C C C K R Q K R T K I R
3421 AGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGACAAAAAGGACTAAATCAG
991 K K T K Y T I L D N M D E Q E R M E L P
3481 GAAAAAACAAGTACACCATCCTGGATAACATGGATGAACAGGAAAGAATGGAAGTGAAG
1011 P K Y G I K R R S T E H N S S L M V S E
3541 GCCCAATATGGTATCAAGCACCGAAGCACAGAGCACAACCTCCAGCCTGATGGTATCCGA
1031 S E F D S D Q D T I F S R E K M E R G N
3601 GTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGAGAAAAGATGGAGAGAGGGAA
1051 P K V S M N G S I R N G A S F S Y C S K
3661 TCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCTTCCTTCAGTTATTGCTCAAA
1071 D R *
3721 GGACAGATAAatggcgagttcattgttaaagtgggaaggacccyttgaatccargaccagtc
3781 agtgggagttacagcacaaaacccactcttttagaatagttcattgaccttcttccccag

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Figure 2A-4

3841 tgggttagatgtgtatccccacgtactaaaaagaccgggtttttgaaggccacaaaaacaaaaa
3901 ctttgctcttttaactgagatgcttggttaatagaaataaaggctgggtaaaaactytaaagg
3961 tatatactttaaagagtttttgagttttttagctggcacaatctcatattaaagatgaac
4021 aacgatttcttatctgtagaacotttagagaagggtgaatgaaacaagggttttaaaaaagggat
4081 gatthctgtcttagcgtgtgattgcctctaaaggaacagcattctaaacacgggtttctc
4141 ttgtaggacctgcagtcagatggctgtgtatgtttaaataagcttgtctaaagaggcaccggg
4201 ccattctgtggaggtacggaggtcttgcatgttagcaagctttctgtgctgaaggcaaacctc
4261 gcacagtgccaagccctcctgggtttttaattctgtgctatgtcaatggcagttttcatct
4321 ctctcaagaaagcagctgttggccattcaagagctaagggaagaatcgtattctaaaggaact
4381 gaggcaatagaaaggggaggaggagcttaatgccttgagggttgaaggtagcattgtaac
4441 attatcttttcttctctaaagaaaaactacactgactcctctcgggtgttgttttagcagta
4501 tagttctctaattgtaaaccrgatccccagttttacatttaartgcaatagaagtgttaattc
4561 attaaagcatttattatgttctgttaggtgtgctgttggactgccatagataggkatakaacg
4621 acacagcaattgtgtatattccaaaaactctgaaatacagtcagtcttaacttggatgg
4681 cgtgggttatgatactctgggtccccgacaggtactttccaaaataacttgacatagatgta
4741 ttcacttcatatgtttaaaaatacatttaagtttttctaccgaataaatcttattttcaaa
4801 catgaaagacaattaaaaacattcccacccacaaaagcagactcccagagcaatttaactgga
4861 gtttaattgtagcctgctacgtttgactgggttcagggttagttcccatccacccttgggtcct
4921 gaggctgggtggccttgggtgggtgaccttggcattttttgtgggaagattagaatgagagat
4981 agaaccagtggtgtggtaccaagtggtgagcacacctaaacaatatcctgttgcacaatgc
5041 ttttttaacacatgggaaaaactaggaatgcattgctgatgaagaagcaagggtattttaaac
5101 accagggcaggagtgccagagaaaaatgtttcccatgggttcttaaaaaaaaaattcagctt
5161 ttaggtgcttttgtcatctcccgagttatcctcctcatgggaccatcttatttttaactt
5221 attgtaatttactggggaaaggcagaactaaaaagtggtgtcatttttatttttaaaaaaat
5281 tgctttgcttatgctacactttctgtataactagccaattcaatactgtctatagtgtt
5341 agaaggaaaaatgtgatttttttttttaaccagttattgagcttcataagcctagaatctg
5401 ccttatcagggtgaccagggttatggttggttgcatgcaaatgtgaattttctggcataggg
5461 gacagcagcccaaatgtaaagtcatogggcgtaattgaggaagaaggaggagtgaaacattttac
5521 cgctttakgtacataacatatgcagtttaacatactcatttgatccttataatcaaccttg
5581 aagaggagatactatcattcttatgttgccagatagccctctgaaggccagagaggttaa
5641 rtaacttcccagaggtcatggccaagaagtagtggtcccaagaactgaatgcaaattttt
5701 taaactgtagagttctgctttccactaaacaaagaactcctgccttgatggatggagggc
5761 aaattctggtggaacttttggggccacctgaaagtcttatccaggactaagaggaattt
5821 cttttaatggatccagagagccaagggtcagaggagagatggcctgcatagtctcctgtg
5881 gatcacacccggggccaccctcctctaggtttacagtggacttctctgccccctcctcc
5941 tttctgtccttggccatctcagcctggcctctctgatccttccatcacagaaggatctt
6001 gaatctctgggaaatcaaacatcacagtagtgatcagaaagtgaagtctgtcttgcacc
6061 ccatttctcatcagaacaaagcaccagagatggaatgaccaaccagcattcttcatgggtgga
6121 ctgcttatcattgaggatctttgggagataaagcacgctaagagctctggacagagaaaa
6181 acaggccctagaatatgggagtggtgtttgtagggtctcayargctaacaagcacttttag
6241 ttgctgggtttacattcaatgaaggaggattcatacccatggcattacaaggcctaagcatg

Figure 2A-5

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6301 tgtatgactaaggaactatctgaaaaacatgcagcaaggtaagaaaatgtaccactcaac
6361 aagccagtgatgccaccttttgtgcgggggaggagagtgaactaccattgttttttgtgt
6421 gacaaagctatcatggactattttaaatcttggttttattgcttaaaatatattatttttc
6481 cctatgtgttgacaaggtatcttaatatcacactatttaaatatatgcactaatotaaat
6541 aaagggtgtctgtatcttctgtaatgcttatttttagggggaaatttgttttctttatgct
6601 tcagggttagagggattcccttgagttaggtcagcaaaactctggcctgcagcctgtgtgt
6661 gcacgccccatgagcogaaaagtgggtcttatgttttcaaatgggttaaaaaataaataaaa
6721 aaatttgaaacatgtgaactatatgacattcagatttgtgttcaataaataaagttttatt
6781 ggaacatatcc

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Figure 2B. The cDNA (SEQ ID NO. : 4) and amino acid sequence (SEQ ID NO. : 5) of 254P1D6B v.2.

The start methionine is underlined. The open reading frame extends from nucleic acid 512-3730 including the stop codon.

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1 gctgcgcggcggtggggcggggatcccccggggtgcaaccttgctccacctgtgtgtgc
61 cctcgggggcctgggtggccccgcgcagagcggcgcgcgctcgtgtcactgccgga
121 ggtgagagcgcagcagtagcttcaagcctgtcttgggcttggtccagattcgctcctctgg
181 ggctacgtccccgggaagaggaagcgcaggattttgctgggggtggggctgtacctctaac
241 agcaggtgcgcgcgcgaggggtgtgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
301 taagacctgcgatgacgacgaggaggaacaagtgggacgcgcagtgatgctcagggccag
361 cagcaacgcctggggcgagcttcagtgctgcgcagcagtgaccacagttcttgaggccaaa
421 tctggctcctaaaaaacatcaaaaggaagcttgcaccaaaactctcttcaggggccgcctcag
1 M A P P T G V L S S
481 aagcctgccatcacccactgtgtgtgtgcacaATGGCGCCCCCACAGGTGTGCTCTCTTC
11 L L L L V T I A G C A R K Q C S E G R T
541 ATTGCTGCTGCTGGTGACAATTGCAGGTTGTGCCCCGTAAGCAGTGACGAGGGGAGGAC
31 Y S N A V I S F N L E T T R I M R V S H
601 ATATTCGAATGCAGTCATTTCACCTAACTTGGAAACCACCAGAATCATGCGGGTGTCTCA
51 T F P V V D C T A A C C D L S S C D L A
661 CACCTTCCCTGTCTGACTGCACGGCCGCTTGCTGTGACCTGTCCAGCTGTGACCTGGC
71 W W F E G R C Y L V S C P H K E N C E P
721 CTGGTGGTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCCCACAAAGAGAACTGTGAGCC
91 K K M G F I R S Y L T F V L R F V Q R P
781 CAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTGCTCCGGCCTGTTTCAGAGGCC
111 A Q L L D Y G D M M L N R G S P S G I W
841 TGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGGGGCTCCCCCTCGGGGATCTG
131 G D S P E D I R K D L P F L G K D W G L
901 GGGGGACTCACCTGAGGATATCAGAAAGGACTTGCCCTTTCTAGGCAAGATTGGGGCCT
151 E E M S E Y A D D Y R E L E K D L L Q P
961 AGAGGAGATGTCTGAGTACGCAGATGACTACCGGGAGCTGGAGAAGGACCTCTTGCAACC
171 S G K Q E P R G S A E Y T D W G L L P G
1021 CASTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACGGACTGGGGCCTACTGCCGGG

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Figure 2B-2

191 S E G A F N S S V G D S P A V P A E T Q
1081 CAGCGAGGGGGCCTTCAACTCCTCTGTTGGAGACAGTCCCTGCGGTGCCAGCGGAGACGCA
211 Q D P E L R Y L N E S A S T P A F K L P
1141 GCAGGACCCTGAGCTCCATTACCTGAATGAGTCGGCTTCAACCCCTGCCCAAACTCCC
231 E R S V L L F L P T T P S S G E V L E K
1201 TGAGAGAAGTGTGTTGCTTCCCTTGGCGACTACTCCATCTTCAGGAGAGGTGTTGGAGAA
251 E K A S Q L Q E Q S S N S S G K E V L M
1261 AGAAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGCTCTGGAAAAGAGGTTCTAAT
271 P S H S L F P A S L E L S S V T V E K S
1321 GCCTTCCCATAGTCTTCCCTCCGGCAAGCCTGGAGCTCAGCTCAGTCACCGTGGAGAAAAG
291 P V L T V T F G S T E H S I P T P F T S
1381 CCCAGTGTCTACAGTCACCCCGGGGAGTACAGAGCACAGCATCCCAACACCTCCCCTAG
311 A A P S E S T P S E L P I S P T T A P R
1441 CGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATATCTCCTACCCTGCTCCCAG
331 T V K E L T V S A G D N L I I T L P D N
1501 GACAGTGAAGAAGAACTTACGGTATCGGCTGGAGATAACCTAATTATAACTTTACCCGACAA
351 E V E L K A F V A P A P P V E T T Y N Y
1561 TGAAGTTGAAGTGAAGGCCTTTGTTGCGCCAGCGCCACCTGTAGAAACAACCTACAATA
371 E W N L I S H P T D Y Q G E I K Q G H K
1621 TGAATGGAATTTAATAAGCCACCCACAGACTACCAAGGTGAAATAAAACAAGGACACAA
391 Q T L N L S Q L S V G L Y V F K V T V S
1681 GCAAACCTCTTAACCTCTCTCAATTGTCCGTCGGACTTTATGTCTTCAAAGTCACTGTTTC
411 S E N A F G E G F V N V T V K P A R R V
1741 TAGTGAAAACGCCTTTGGAGAAGGATTTGTCAATGTCAGTGTAAAGCCTGCCAGAAGAGT
431 N L P F V A V V S P Q L Q E L T L P L T
1801 CAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAAGAGCTCACTTTGCCTTTGAC
451 S A L I D G S Q S T D D T E I V S Y H W
1861 GTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACTGAAATAGTGAGTTATCATTG
471 E E I N G P F I E E K T S V D S P V L R
1921 GGAAGAAATAAACGGGCCCTTCATAGAAGAGAAGACTTCAGTTGACTCTCCCGTCTTACG
491 L S N L D P G N Y S F R L T V T D S D G
1981 CTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTGACTGTACAGACTCGGACGG
511 A T N S T T A A L I V N N A V D Y P P V
2041 AGCCACTAAGTCTACAAGTGCAGCCCTAATAGTGAACAATGCTGTGGACTACCCACCACT
531 A N A G P N H T I T L P Q N S I T L N G
2101 TGCTAATGCAGGACCAAATCACACCATAACTTTGCCCAAACTCCATCACTTTGAATGG
551 N Q S S D D H Q I V L Y E W S L G F G S
2161 AAACCAGAGCAGTGACGATCACCAGATTGTCTCTATGAGTGGTCCCTGGGTCTGGGAG
571 E G K H V V M Q G V Q T F Y L H L S A M
2221 TGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCATACCTTCATTTATCTGCAAT
591 Q E G D Y T F Q L K V T D S S R Q Q S T

Figure 2B-3

2281 GCAGGAAGGAGATTATACATTTTCAGCTGAAGGTGACAGATTCTTCAAGGCAACAGTCTAC
611 A V V T V I V Q P E N N R P P V A V A S
2341 TGCTGTAGTGAAGTGTGATTGTCCAGCCTGAAAACAATAGACCTCCAGTGGCTGTGGCCGG
631 P D K E L I F P V E S A T L D G S S S S
2401 CCCTGATAAAGAGCTGATCTTCCCAGTGGAAAGTGCTACCCCTGGATGGGAGCAGCAGCAG
651 D D H G I V F Y H W E H V R G P S A V E
2461 CGATGACCACGGCATTGTCTTCTACCACTGGGAGCAGCTCAGAGGCCCCAGTGCAGTGGGA
671 M E N I D K A I A T V T G L Q V G T Y H
2521 GATGGAAAATATTGACAAAGCAATAGCCACTGTGACTGGTCTCCAGGTGGGGACCTACCA
691 F R L T V K D Q Q G L S S T S T L T V A
2581 CTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGCAGCTCCACCCTCACTGTGGC
711 V K K E N N S P P R A R A G G R H V L V
2641 TGTGAAGAAGGAAAATAATAGTCCTCCAGAGCCCCGGGCTGGTGGCAGACATGTTCTTGT
731 L P N N S I T L D G S R S T D D Q R I V
2701 GCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCTACTGATGACCAAAGAATTGT
751 S Y L W I R D G Q S P A A G D V I D G S
2761 GTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCTGGAGATGTCATCGATGGCTC
771 D H S V A L Q L T N L V E G V Y T F H L
2821 TGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAGGGGGTGTACACTTTCCACTT
791 R V T D S Q G A S D T D T A T V E V Q P
2881 GCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACTGCCACTGTGGAAGTGCAGCC
811 D P R K S G L V E L T L Q V G V G Q L T
2941 AGACCCTAGGAAGAGTGGCCTGGTGGAGCTGACCCTGCAGGTTGGTGTGGGCAGCTGAC
831 E Q R K D T L V R Q L A V L L N V L D S
3001 AGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTGCTGCTGAACGTGCTGGACTC
851 D I K V Q K I R A H S D L S T V I V F Y
3061 GGACATTAAGGTCCAGAAGATTCCGGCCCCACTCCGATCTCAGCACCGTGATTGTGTTTTA
871 V Q S R P P F K V L K A A E V A R N L H
3121 TGTACAGAGCAGGCCGCCCTTTCAAGGTTCTCAAAGCTGCTGAAGTGGCCCCGAAATCTGCA
391 M R L S K E K A D F L L F K V L R V D T
3181 CATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTCAAGGTCTTGAGGGTTGATAC
911 A G C L L K C S G H G H C D P L T K R C
3241 AGCAGGTTGCCTTCTGAAGTGTCTGGCCATGGTCACTGCGACCCCTCACAAGCGCTG
931 I C S H L W M E N L I Q R Y I W D G E S
3301 CATTTGCTCTCACTTATGGATGGAGAACCCTTATACAGCGTTATATCTGGGATGGAGAGAG
951 N C E W S I F Y V T V L A F T L I V L T
3361 CAACTGTGAGTGGAGTATATTCTATGTGACAGTGTGGCTTTTACTCTTATTGTGCTAAC
971 G G F T W L C I C C C K R Q K R T K I R
3421 AGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGACAAAAAGGACTAAAATCAG
991 K K T K Y T I L D N M D E Q E R M E L R
3481 GAAAAAACAAGTACACCATCCTGGATAACATGGATGAACAGGAAAGAATGGAAGTGAAG

Figure 2B-4

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1011 P K Y G I R H R S T E H N S S L M V S E
3541 GCCCAAATATGGTATCAAGCACCGAAGCACAGAGCACAAC'TCCAGCCTGATGGTATCCGA
1031 S E F D S D Q D T I F S R E K M E R G N
3601 GTCTGAGTTTGACAGTGACCAGGACACAATCTTTCAGCCGAGAAAAGATGGAGAGAGGGAA
1051 P K V S M N G S I R N G A S F S Y C S K
3661 TCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCTTCCTTCAGTTATTGCTCAAA
1071 D R *
3721 GGACAGATAAtggcgcagttcattgtaaagtgggaaggacccottgaatccaagaccagtc
3781 agtgggaggttacagcacaaaaacccactctttttagaatagttcattgaccttcttcccccag
3841 tgggttagatgtgtatccccacgtactaaaagaccggtttttgaaggcacaaaaacaaaaa
3901 ctttgctcttttaactgagatgcttgttaabagaaataaaggctgggtaaaaactctaagg
3961 tatatacttaaaagagttttgagttttttagtctggcacaatctcatattaaagatgaac
4021 aacgattttctatctgtagaacotttagagaaggtgaatgaaacaagggttttaaaaaaggat
4081 gatttctgtcttagccgctgtgattgcctctaagggaacagcattctaaacacgggtttctc
4141 ttgtaggacctgcagtcagatggctgtgtatgttbaaaatagcttgtctaagaggcacagg
4201 ccactctgtggaggtacggagtccttgcagtagcaagctttctgtgctgacgggaacactc
4261 gcacagtgccaagccctcctgggtttttaattctgtgctatgtcaatggcagttttcatct
4321 ctctcaagaaagcagctgttgccattcaagagctaagggaagaatcgtattctaaggact
4381 gaggcaatagaaaaggggaggaggagcttaatgccgtgcaggttgaaggtagcattgtaac
4441 attatcttttctttctctaagaaaaactacactgactcctctcgggtgttgttttagcagta
4501 tagttctctaattgtaaacggatccccagttttacattaaatgcaatagaagtgttaattc
4561 attaacgatttattatgttctgtaggctgtgcgttttggaactgccatagatagggataacg
4621 actcagcaattgtgtatatattccaaaactctgaaatacagtcagtccttaacttggatgg
4681 cgtgggttatgatactctgggtcccccagaggtactttccaaaataacttgacatagatgta
4741 ttcacttcatatgtttaaaaatacatttaagtttttctaccgaataaaatcttattttcaa
4801 catgaaagacaattaaaaacattcccacccacaaaagcagtcactcccagcaattaaactgga
4861 gtttaattgtagcctgctacgttgactgggttcagggtagttcccatccaccccttggctct
4921 gaggtgtgtggccttgggtgggtgccccttggcattttttgtgggaagattagaatgagagat
4981 agaaccagtggtgtggtaccaagtgtgagcacacctaacaatatacctgttgcaaatgc
5041 ttttttaacacatgggaaaaactaggaatgcattgctgatgaagaagcaagggtatttaaac
5101 accagggcaggagtgccagagaaaaatgtttcccatgggttcttaaaaaaaattcagctt
5161 ttaggtgcttttgtcatctcccgaggtattcatcctcatgggaccatcttatttttactt
5221 attgtaatttactggggaaaggcagaactaaaaagtggtgtcattttatttttaaaataat
5281 tgctttgcttatgcctacactttctgtataaactagccaattcaatactgtctatagtgtt
5341 agaaggaaaatgtgatttttttttttaaccagbattgagcttcataagcctagaatctg
5401 ccttatcaggtgaccaggggttatgggtgtttgcatgcaaatgtgaatttctggcataggg
5461 gacagcagcccaaatgtaaaagtcacgggogtaatgaggaagaaggagtgaaacatttac
5521 cgctttatgtacataacatattgcagtttacatactcatttgatccttataatcaaccttg
5581 aagaggagatactatcattcttatgttgcagatagccctctgaaggcccagagaggttaa
5641 gtaacttccagaggtcatggccaagaagtagtggtcccaagaactgaatgcaaatTTTT
5701 taaactgtagagttctgctttccactaaacaaagaactcctgccttgatggatggagggc

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Figure 2B-5

5761 aaattctggtggaacttttggggccacctgaaagtcttatccaggactaagaggaattt
5821 cttttaatggatccagagagccaagggtcagagggagagatggcctgcatagtctcctgtg
5881 gatcacacccggggcccccctccctctaggtttacagtggacttcttctgccccctcctcc
5941 tttctgtccttggccatctcagcctggcctctctgatccttccatcagagaaggatctt
6001 gaatctctgggaaatcaaacatcacagtagtgatcagaaagtgagtctctgtcttgtcacc
6061 ccatttctcatcagaacaaagcacgagatggaatgaccaaccagcattcttcatgggtgga
6121 cggcttatcattgaggatctttgggagataaagcacgctaagagctctggacagagaaaa
6181 acaggccctagaatatgggagtggtgtttgttagggctcataggctaacaagcacttttag
6241 ttgctggtttacattcaatgaaggaggattcatacccatggcattacaaggctaagcatg
6301 tgtatgactaaggaactatctgaaaaacatgcagcaaggtaagaaaatgtaccactcaac
6361 aagccagtgatgccaccttttgtgcgcggggaggagagtgactaccattgttttttgtgt
6421 gacaaagctatcatggactattttaattcttggttttattgcttaaaatatattatttttc
6481 cctatgtgttgacaaggatatttctaataatcacactattaaatatatgcactaatctaaat
6541 aaaggtgtcgtattttctgtaaatgcttatttttagggggaaatttgttttctttatgct
6601 tcagggttagagggttcccttgagtatagggtcagcaaacctctggcctgcagcctgtgtgt
6661 gcacgccccatgagccgaaaagtgggtcttatgttttcaaatgggttaaaaaataaataaaa
6721 aaatttgaaacatgtgaactatatgacattoagatttgggttcataaataaagttttatt
6781 ggaacatatcc

Figure 2C. The cDNA (SEQ ID NO. : 6) and amino acid sequence (SEQ ID NO. : 7) of 254P1D6B v.3.

The start methionine is underlined. The open reading frame extends from nucleic acid 739-3930 including the stop codon.

1 gctgccgcggggcggtggggggggatcccccgggggtgcaacottgctccacctgtgtctgc
61 cctcggggggcctgggtggccccgcgcagagcgggcgggcgctcgtgtcactgccggga
121 ggtgagagcgccagcagtagcttcagcctgtcttgggcttggtccagattcgctcctctgg
181 ggctacgtcccggggaagaggaagcgaggattttgctgggggtggggctgtacctottaac
241 agcagggtgcgcgcgcgaggggtgtgaacgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt
301 taagacctgogatgaagcagaggaggaacaagtgggacggcgagtgatgctcagggccag
361 cagcaacgcctggggcgagcttcagtgtcgcagcagtgaccacaggtacgggtatctact
421 tcccagagcgccctggccgagaaataggaaagagggcagccagtaggcaggccaataccca
481 acaaaagtagaatcgagacgccccgtgagttcagaagttcttgaggccaaatctggctccta
541 aaaaacatcaaaggaagcttgcaaaaaactctcttcagggccgcctcagaagcctgccat
601 caccactgtgtggtgcacaatggcgccccccacaggtgtgtctctcttcattgtgtgtgc
661 tgggtgacaattgcagtttgcattatgggtggatgcactcatggcaaaaaaatcactgggtgag
1 M T R L G W P S P C C A R K
721 catcatttaagaagacccATGACTAGACTGGGCTGGCCGAGCCCATGTTGTGCCCGTAAG
15 Q C S E G R T Y S N A V I S P N L E T T
781 CAGTGCAGCGAGGGGAGGACATATTCCAATGCAGTCATTTCACCTAACTTGGAAACCACC
35 R I M P V S H T F F V V D C T A A C C D
841 AGAATCATGCGGGTGTCTCACACCTTCCCTGTCTGCTAGACTGCACGGCCGCTTGTCTGTGAC
55 L S S C D L A W W F E G R C Y L V S C P

Figure 2C-2

901 CTGTCCAGCTGTGACCTGGCCTGGTGGTTTCGAGGGCCGCTGCTACCTGGTGAGCTGCCCC
75 H K E N C E P K K M G P I R S Y L T F V
961 CACAAAGAGAACTGTGAGCCCCAAGAAGATGGGCCCCATCAGGTCTTATCTCACTTTTGTG
95 L R P V Q R P A Q L L D Y G D M M L N R
1021 CTCCGGCCTGTTTCAGAGGCCTGCACAGCTGCTGGACTATGGGGACATGATGCTGAACAGG
115 G S P S G I W G D S P E D I R K D L P F
1081 GGCTCCCCCTCGGGGATCTGGGGGGACTCACCTGAGGATATCAGAAAGGACTTGCCCTTT
135 L G K D W G L E E M S E Y S D D Y R E L
1141 CTAGGCAAAGATTGGGGCCTAGAGGAGATGTCTGAGTACTCAGATGACTACCGGGGAGCTG
155 E K D L L Q P S G K Q E P R G S A E Y T
1201 GAGAAGGACCTCTTGCAACCCAGTGGCAAGCAGGAGCCCAGAGGGAGTGCCGAGTACACG
175 D W G L L P G S E G A F N S S V G D S P
1261 GACTGGGGCCTACTGCCGGGCAGCGAGGGGGCCCTTCAACTCCTCTGTTGGAGACAGTCCT
195 A V P A E T Q Q D P E L H Y L N E S A S
1321 GCGGTGCCAGCGGAGACGCAGCAGGACCCCTGAGCTCCATTACCTGAATGAGTCGGCTTCA
215 T P A P K L P E R S V L L P L P T T P S
1381 ACCCCTGCCCCAAACTCCCTGAGAGAAGTGTGTTGCTTCCCTTGCCGACTACTCCATCT
235 S G E V L E K E K A S Q L Q E Q S S N S
1441 TCAGGAGAGGTGTTGGAGAAAAGAAAGGCTTCTCAGCTCCAGGAACAATCCAGCAACAGC
255 S G K E V L M P S H S L P P A S L E L S
1501 TCTGGAAAAGAGGTTCTAATGCCTTCCCATAGTCTTCCCTCCGGCAAGCCTGGAGCTCAGC
275 S V T V E K S P V L T V T P G S T E H S
1561 TCAGTCACCGTGGAGAAAAGCCCAGTGCCTCACAGTCACCCCGGGGAGTACAGAGCACAGC
295 I P T P P T S A A P S E S T P S E L P I
1621 ATCCCAACACCTCCCCTAGCGCAGCCCCCTCTGAGTCCACCCCATCTGAGCTACCCATA
315 S P T T A P R T V K E L T V S A G D N L
1681 TCTCCTACCACTGCTCCCAGGACAGTGAAAGAACTTACGGTATCGGCTGGAGATAACCTA
335 I I T L P D N E V E L K A F V A P A P P
1741 ATTATAACTTTACCCGACAATGAAGTTGAACTGAAGGCCCTTTGTTGGCGCCAGCGCCACCT
355 V E T T Y N Y E W N L I S H P T D Y Q G
1801 GTAGAAACAACCTACAACCTATGAATGGAATTTAATAAGCCACCCACAGACTACCAAGGT
375 E I K Q G H K Q T L N L S Q L S V G L Y
1861 GAAATAAAACAAGGACACAAGCAAACCTCTTAACCTCTCTCAATTGTCCGTCCGACTTTAT
395 V F K V T V S S E N A F G E G F V N V T
1921 GTCTTCAAAGTCACTGTTTCTAGTGAAAACGCCCTTTGGAGAAGGATTTGTCAATGTCACCT
415 V K P A R R V N L P P V A V V S P Q L Q
1981 GTTAAGCCTGCCAGAAGAGTCAACCTGCCACCTGTAGCAGTTGTTTCTCCCCAACTGCAA
435 E L T L P L T S A L I D G S Q S T D D T
2041 GAGCTCACTTTGCCTTTTGACGTCAGCCCTCATTGATGGCAGCCAAAGTACAGATGATACT
455 E I V E Y H W E E I N G P F T E E K T S
2101 GAAATAGTGAGTTATCATTGGGAAGAAATAAACGGGGCCCTTCATAGAAGAGAAGACTTCA

Figure 2C-3

475 V D S P V L R L S N L D P G N Y S F R L
2161 GTTGACTCTCCCGTCTTACGCTTGTCTAACCTTGATCCTGGTAACTATAGTTTCAGGTTG
495 T V T D S D G A T N S T T A A L I V N N
2221 ACTGTTACAGACTCGGACGGAGCCACTAACTCTACAACCTGCAGCCCTAATAGTGAACAAT
515 A V D Y P P V A N A G P N H T I T L P Q
2291 GCTGTGGACTACCCACCAGTTGCTAATGCAGGACCAAATCACACCATAACTTTGCCCCAA
535 N S I T L N G N Q S S D D H Q I V L Y E
2341 AACTCCATCACTTTGAATGGAAACCAGAGCAGTGACGATCACCAGATTGTCCTCTATGAG
555 W S L G P G S E G K H V V N Q G V Q T F
2401 TGGTCCCTGGGTCCTGGGAGTGAGGGCAAACATGTGGTCATGCAGGGAGTACAGACGCCA
575 Y L H L S A M Q E G D Y T F Q L K V T D
2461 TACCTTCATTTATCTGCAATGCAGGAAGGAGATTATACATTTTCAGCTGAAGGTGACAGAT
595 S S R Q Q S T A V V T V I V Q P E N N R
2521 TCTTCAAGGCAACAGTCTACTGCTGTGGTGACTGTGATTGTCCAGCCTGAAAACAATAGA
615 F P V A V A G P D K E L I F P V E S A T
2581 CCTCCAGTGGCTGTGGCCGGCCCTGATAAAGAGCTGATCTTCCAGTGGAAAGTGCTACC
635 L D G S S S S D D H G I V F Y H W E H V
2641 CTGGATGGGAGCAGCAGCAGCGATGACCACGGCATTGTCTTCTACCACTGGGAGCACGTC
655 R G P S A V E M E N I D K A I A T V T G
2701 AGAGGCCCCAGTGCAGTGGAGATGCAAAATATTGACAAAGCAATAGCCACTGTGACTGGT
675 L Q V G T Y H F R L T V K D Q Q G L S S
2761 CTCCAGGTGGGACCTACCACTTCCGTTTGACAGTGAAAGACCAGCAGGGACTGAGCAGC
695 T S T L T V A V K K E N N S P P R A R A
2821 ACGTCCACCCTCACTGTGGCTGTGAAGAAGGAAAATAATAGTCCTCCAGAGCCCGGGCT
715 G G R H V L V L P N N S I T L D G S R S
2881 GGTGGCAGACATGTTCTTGTGCTTCCCAATAATTCCATTACTTTGGATGGTTCAAGGTCT
735 T D D Q R I V S Y L W I R D G Q S P A A
2941 ACTGATGACCAAGAATTGTGTCCTATCTGTGGATCCGGGATGGCCAGAGTCCAGCAGCT
755 G D V I D G S D H S V A L Q L T N L V E
3001 GGAGATGTCATCGATGGCTCTGACCACAGTGTGGCTCTGCAGCTTACGAATCTGGTGGAG
775 G V Y T F H L R V T D S Q G A S D T D T
3061 GGGGTGTACACTTTCCACTTCCGAGTCACCGACAGTCAGGGGGCCTCGGACACAGACACT
795 A T V E V Q P D P R K S G L V E L T L Q
3121 GCCACTGTGGAAGTGCAGCCAGACCCTAGGAAGAGTGGCCTGGTGGAGCTGACCCTGCAG
815 V G V G Q L T E Q R K D T L V R Q L A V
3181 GTTGGTGTGGGAGCTGACAGAGCAGCGGAAGGACACCCTTGTGAGGCAGCTGGCTGTG
835 L L N V L D S D I K V Q K I R A H S D L
3241 CTGCTGAACGTGCTGGACTCGGACATTAAGGTCCAGAAGATTTCGGGCCCACTCGGATCTC
855 S T V I V F Y V Q S R P P F K V L K A A
3301 AGCACCGTGATTGTGTTTTATGTACAGAGCAGCGCCGCTTTCAAGGTTCTCAAAGCTGCT
875 E V A R N L H M R L S K E K A D F L L F

Figure 2C-4

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3361 GAAGTGGCCCGAAATCTGCACATGCGGCTCTCAAAGGAGAAGGCTGACTTCTTGCTTTTC
895 K V L R V D T A G C L L K C S G H G H C
3421 AAGGTCCTTGAGGGTTGATACAGCAGGTTGCCCTTCTGAAGTGGTTCTGGCCATGGTCACTGC
915 D F L T K R C I C S H L W M E N L I Q R
3481 GACCCCTCACAAGCGCTGCATTTGCTCTCACTTATGGATGGAGAACCTTATACAGCGT
935 Y I W D G E S N C E W S I F Y V T V L A
3541 TATATCTGGGATGGAGAGAGCAACTGTGAGTGGAGTATATCTATGTGACAGTGTGGCT
955 F T L I V L T G G F T W L C I C C C K R
3601 TTTACTCTTATTGTGCTAACAGGAGGTTTCACTTGGCTTTGCATCTGCTGCTGCAAAAGA
975 Q K R T K I R K K T K Y T I L D N M D E
3661 CAAAAAGGACTAAAATCAGGAAAAAAACAAAGTACACCATCCTGGATAACATGGATGAA
995 Q E R M E L R P K Y G I K H R S T E H N
3721 CAGGAAAGAATGGAAGTGGAGGCCCCAAATATGGTATCAAGCACCAGACAGAGCACAAC
1015 S S L M V S E S E F D S D Q D T I F S R
3781 TCCAGCCTGATGGTATCCGAGTCTGAGTTTGACAGTGACCAGGACACAATCTTCAGCCGA
1035 E K M E R G N P K V S M N G S I R N G A
3841 GAAAAGATGGAGAGAGGGAATCCAAAGGTTTCCATGAATGGTTCCATCAGAAATGGAGCT
1055 S F S Y C S K D R *
3901 TCCTTCAGTTATTGCTCAAAGGACAGATAAatggcgcagttcattgttaaagtgyaaggacc
3961 ccttgaatccaagaccagtcagtgagggttacagcacaaaaccactcttttagaatagt
4021 tcattgacottcttccccagtgagggttagatgtgtatccccacgtactaaaagaccggttt
4081 ttgaaggcacaaaaacaaaaactttgtcttttaactgagatgcttgttaatatagaaataaaa
4141 ggctgggtaaaactctaaggtatataacttaaaagagttttgagtttttgtagctggcaca
4201 atctcatattaaagatgaacaaacgattttctatctgtagaaccttagagaaggtgaatgaa
4261 acaagggttttaaaaagggtatgattttctgtcttagccgctgtgattgootctaagggaacag
4321 cattctaaacacgggtttctcttgtaggacctgcagtcagatggctgtgtatgttaaaata
4381 gcttgtctaaagaggcaacgggcatctgtggaggtacggagtccttgcatgtagcaagcttt
4441 ctgtgctgaaggcaacactgcacagtgccaagccctcctgggttttaattctgtgtat
4501 gtcaatggcagttttcatctctctcaagaaagcagctgttggccattcaagagctaagga
4561 agaatcgtattctaaggactgaggcaatagaaaggggaggaggagcttaatgccgtgcag
4621 gttgaaggtagcattgttaacattatcttttctcttaagaaaaactacactgaactcct
4681 ctccggtgtgttttagcagtatagttctctaatgtaaacggatccccagtttacattaaat
4741 gcaatagaagtgttaattcattaagcatttattatgttctgtaggctgtgcgtttggac
4801 tgccatagatagggataaacgactcagcaattgtgtatatattccaaaactctgaaataca
4861 gtcagtccttaacttggtatggcgtgggttatgatactctgggtccccgacaggtactttccaa
4921 aataacttgacatagatgtattcacttcatatgttttaaaaatacatttaagtttttctac
4981 cgaataaatcttattttcaaacatgaaagacaattaaaaacattcccaccacaaaagcagta
5041 ctcccgagcaatthaactggaggttaattgttagcctgctaogttgactgggttcagggttagtt
5101 ccccatccacccttggtcctgagggtggtggccttggtgggtgcccttggcattttttgtg
5161 ggaagattagaatgagagatagaaccagtggtgtgtgtaccgaagtgtgagcacacctaacc
5221 aatatcctgttgcacaatgcttttttaacacatgggaaaaactaggaatgcattgctgatg

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Figure 2C-5

5281 aagaagcaagggtattttaaacaccagggcaggagtgcagagagaaaatgtttcccatgggt
5341 tcttaaaaaaattcagcttttaggtgcttttgatctctccggagtattcactctcatg
5401 ggaccatcttatttttaacttattgttaatttactggggaaaggcagaactaaaaagtgtgt
5461 cattttatttttaaaataatttgctttgcttatgcttacactttctgtataactagccaat
5521 tcaatactgtctatagtgttagaaggaaaaatgtgatttttttttttaaccagtattgag
5581 cttcataagcctagaatctgccttatcagggtgaccaggggttatgggtgtttgcatgcaaa
5641 tgtgaattttctggcataggggacagcagcccaaatgtaaagtcatcgggogtaattgagga
5701 agaaggaggtgaacatttaccgcttttatgtacataacatattgcagtttacatactcattt
5761 gatcctttataatcaacottgaagaggagatactatcattcttatgtttgcagatagccctc
5821 tgaaggccagagaggttaagtaacttccagaggtcatggccaagaagttagtggctcca
5881 agaactgaatgcaaattttttaactgttagagttcttgctttccactaaacaaagaactcc
5941 tgctttgatggatggaggggcaaatcttggtggaaacttttggggccacctgaaagtctatt
6001 cccaggactaagaggaattttcttttaattggatccagagagccaagggtcagagggagagat
6061 ggcttgcatagtctctgtggatcacacccggggccacccctccctctaggtttacagtgg
6121 acttctttctgcccctcctcctttttctgtccttgggcatctcagcctggcctctctgatcc
6181 ttccatcacagaaggatcttgaatctctgggaaatcaaacatcacagtagtgatcagaaa
6241 gtgagtcctgtcttggtcaccccatcttctcatcagaacaaagcacgagatggaatgaccaa
6301 ccagcattcttcatgggtggaotgotttatcattgaggatctttgggagataaaagcacgcta
6361 agagctctggacagagaaaaacaggccctagaatatgggagtgggtgtttgtagggtca
6421 taggctaacaagcacttttagttgctggtttacattcaatgaaggaggattcataccatg
6481 gcattacaaggctaagcatgtgtatgactaaggaaactatctgaaaaacatgcagcaagg
6541 aagaaaatgtaccactcaacaagccagtgatgccaccttttgtgcgcggggaggagagtg
6601 actaccattgtttttgtgtgacaaagctatcatggactattttaactcttggttttattg
6661 cttaaaatatattttttccctatgtgttgacaaggatatttctaataatcacactattaa
6721 atatatgcactaatctaaataaaagggtgtctgtattttctgtaatgcttatttttagggg
6781 aaatttgttttctttatgcttcagggttagagggattcccttgagtataggtcagcaact
6841 ctggcctgcagcctgtgtgtgcacgccccatgagccgaaaagtgggtcttatgttttcaa
6901 atggttaaaaataaaataaaaaaatttgaaacatgtgaactatatgacattcagattttgtg
6961 ttcataaataaagttttatttgaacatatcc

Figure 2D. 254P1D6B v.4 through v.20, SNP variants of 254P1D6B v.1. The 254P1D6B v.4 through v.20 proteins have 1072 amino acids. Variants 254P1D6B v.4 through v.20 are variants with single nucleotide difference from 254P1D6B v.1. 254P1D6B v.5 and v.6 proteins differ from 254P1D6B v.1 by one amino acid. 254P1D6B v.4 and v.7 through v.20 proteins code for the same protein as v.1. Though these SNP variants are shown separately, they can also occur in any combinations and in any of the transcript variants listed above in Figures 2A, Figure 2B and Figure 2C.

Variant	Nucleic acid position	Nucleic Acid Variation	Amino Acid Position	Amino Acid Variation
254P1D6B v.4	286	C/G	<i>Silent variant</i>	
254P1D6B v.5	935	C/A	142	P=>T
254P1D6B v.6 (Identical AA as v.2)	980	T/G	157	S=>A
254P1D6B v.7	2347	G/A	<i>Silent variant</i>	
254P1D6B v.8	3762	C/T	<i>Silent variant</i>	
254P1D6B v.9	3772	A/G	<i>Silent variant</i>	
254P1D6B v.10	3955	C/T	<i>Silent variant</i>	
254P1D6B v.11	4096	C/T	<i>Silent variant</i>	
254P1D6B v.12	4415	G/A	<i>Silent variant</i>	
254P1D6B v.13	4519	G/A	<i>Silent variant</i>	
254P1D6B v.14	4539	A/G	<i>Silent variant</i>	
254P1D6B v.15	4614	G/T	<i>Silent variant</i>	
254P1D6B v.16	5184	G/C	<i>Silent variant</i>	
254P1D6B v.17	5528	T/G	<i>Silent variant</i>	
254P1D6B v.18	5641	G/A	<i>Silent variant</i>	
254P1D6B v.19	6221	T/C	<i>Silent variant</i>	
254P1D6B v.20	6223	G/A	<i>Silent variant</i>	

Figure 3:

Figure 3A. Amino acid sequence 254P1D6B v.1 clone LCP-3 (SEQ ID NO. : 8). The 254P1D6B v.1 clone LCP-3 protein has 1072 amino acids.

```

1  MAPPTGVLSS LLLLVTIAGC ARKQCSEGRY YSNAVISPNI ETTRIMRVSH TFPVVDCTAA
61  CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPFRSYL TFVLRPVQRF AQLLDYGDMM
121 LNRGSPSGIW GDSPEDIRKD LPFLGKDWGL EEMSEYSDY RELEKDLLQF SGKQEPGRSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPELHYLNE SASTPAPKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLDPN EVELKAFVAP
361 APPVETTYNY EWNLSHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDTEIVSYHW EEINGPFIEE
481 KTSVDSPLVR LSNLDPGNYS FRLTVTDSOG ATNSTTAALI VNNAVDPFPV ANAGPNHTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLGPES EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQQST AVVTVIVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
661 EHVRGFSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIY SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADE
901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KTKYTILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSQDQTI FSREKMERGN PKVSMNGSIR NGASFYSYCSK DR

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Figure 3B. Amino acid sequence 254P1D6B v.2 (SEQ ID NO.: 9). The 254P1D6B v.2 protein has 1072 amino acids.

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1  MAPPTGVLSS LLLLVTIAGC ARKQCSEGRY YSNAVISPNI ETTRIMRVSH TFPVVDCTAA
61  CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPFRSYL TFVLRPVQRF AQLLDYGDMM
121 LNRGSPSGIW GDSPEDIRKD LPFLGKDWGL EEMSEYADDY RELEKDLLQF SGKQEPGRSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPELHYLNE SASTPAPKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLDPN EVELKAFVAP
361 APPVETTYNY EWNLSHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDTEIVSYHW EEINGPFIEE
481 KTSVDSPLVR LSNLDPGNYS FRLTVTDSOG ATNSTTAALI VNNAVDPFPV ANAGPNHTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLGPES EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQQST AVVTVIVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
661 EHVRGFSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIY SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADE
901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT

```

Figure 3B-2

961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KTKYTILDN MDEQERMELR PKYGIKIRST
1021 EHNSSLMVSE SEFDSQDQTI FSREKMERGN PKVSMNGSIR NGASFYSYCSK DR

Figure 3C. Amino acid sequence 254P1D6B v.3 (SEQ ID NO: 10). The 254P1D6B v.3 protein has 1063 amino acids.

1 MTRLGWSPSPC CARQKQCEGR TYSNAVISPN LETTRIMRVS HTFPVVDCTA ACCDLSSCDL
61 ANWFEGRCYL VSCPHKENCE PKKMGPIRSY LTFVLRPVQR PAQLLDYGDM MLNRGSPSGI
121 WGDSPEDIRK DLPFLGKDWG LEEMSEYSDD YRELEKDLLQ PSGKQEPGRS AEYTDWGLLP
181 GSEGAFFNSSV GDSPAVPAET QQDPFLHYLN ESASTPAPKL PERSVLLPLP TTPSSGEVLE
241 KEKASQLQEQ SSNSGKEVL MPSSSLPPAS LELSSVTVER SPVLTVTGPS TEHSIPTFPT
301 SAAPSESTPS ELPISPTTAP RTVKELTVSA GDNLIITLPL NEVELKAFVA PAPPVETTYN
361 YEWNLISHPT DYQGEIKQGH KQTLNLSQLS VGLYVFKVTV SSENAFGEGF VNVTVKPARR
421 VNLPPVAVVS PQLQELTLPL TSALIDGSQS TDDTEIVSYH WEEINGPFIE EKTSVDSFVL
481 PLSNLDPGNY SFRLTVTDSG GATNSTTAAL IVNNAVDPYP VANAGPNHTI TLPQNSITLN
541 GNQSSDDHQI VLYEWSLPGS SEGKHVVMQG VQTPYLHLSA MQEGDYTFQL KVTDSRQQS
601 TAVVTIVVQP ENNRPPVAVA GPDKELIFFV ESATLDGSSS SDDHGIVFYH WEHVRGPSAV
661 EMENIDKAIAT TVTGLQVGTY HFRLTVKDQQ GLSSTSTLTV AVKKENNSPP RARAGGRHVL
721 VLPNNSITLD GSRSTDDQRI VSYLWIRDGQ SPAAGDVIDG DHSVALQLT NLVEGVYTFH
781 LRVTDSQGAS DTDATVEVQ PDPRKSGLVE LTLQVGVGQL TEQRKDTLVR QLAVLLNVLD
841 SDIKVQKIRA HSDLSTVIVF YVQSRPPFKV LKAAEVARNL HMRLSKEKAD FLLFKVLRVD
901 TAGCLLKCSG HGHCDPLTKR CICSILWMEN LIQRYIWDGE SNCEWSIFYV TVLAFTLIVL
961 TGGFTWLCIC CCKRQKRTKI RKKTKYTILD NMDEQERMEL RPKYGIKIRS TEHNSSLMVS
1021 ESEFDSQDQI FFSREKMERG NPKVSMNGSI RNASFYSYCS KDR

Figure 3D. Amino acid sequence 254P1D6B v.5 (SEQ ID NO: 11). The 254P1D6B v.5 protein has 1072 amino acids.

1 MAPPTGVLSS LLLLVTIAGC ARKQKQCEGR TYSNAVISPN LETTRIMRVSH TFPVVDCTAA
61 CCDLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPISYLV TFLVRPVQRP AQLLDYGDM
121 LNRGSPSGIW GDSPEDIRKD LTFGLGKDWGL EEMSEYSDDY RELEKDLLQP SGKQEPGRSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPFLHYLNE SASTPAPKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLPPASL ELSSVTVEKS PVLTVTPGST
301 EHSIPTFPTS AAPSESTPSE LPISTPTAPR TVKELTVSAG DNLIITLPLD NEVELKAFVAP
361 APPVETTYNY EWNLISHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDEIVSYHW EEINGPFIEE
481 KTSVDSFVLR LSNLDPGNYS FRLTVTDSG ATNSTTAALI VNNNAVDPYPV ANAGPNHTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLPGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQGST AVVTIVVQPE NNRPPVAVAG PDKELIFFVE SATLDGSSSS DDHGIVFYHW
661 EHVRGPSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTV VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDDQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDI DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLH MRLSKEKADF

Figure 3D-2

901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KTKYITILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSQDQTI FSREKMERGN PKVSMNGSIR NGASFYSYCSK DR

Figure 3E. Amino acid sequence 254P1D6B v.6 (SEQ ID NO: 12). The 254P1D6B v.6 protein has 1072 amino acids.

1 MAPFTGVLSS LLLLVTIAGC ARKQCSEGRF YSNAVITSPNL ETTRIMRVSH TFPVVDCTAA
61 CCCLSSCDLA WWFEGRCYLV SCPHKENCEP KKMGPFRSYL TFVLRPVQRP AQLLDYGDMM
121 INRGSPSGIW GDSPEDIRKD LPFLGKDWGL EEMSEYADDY RELEKDLLQP SGKQEPGRSA
181 EYTDWGLLPG SEGAFNSSVG DSPAVPAETQ QDPHELHYLN SASTPAFKLP ERSVLLPLPT
241 TPSSGEVLEK EKASQLQEQS SNSSGKEVLM PSHSLFPASL ELSSVTVEKS PVLTVTPGST
301 EHSIPTPPTS AAPSESTPSE LPISPTTAPR TVKELTVSAG DNLIITLDPN EVELKAFVAP
361 APPVETTYNY EWNLSHPTD YQGEIKQGHK QTLNLSQLSV GLYVFKVTVS SENAFGEGFV
421 NVTVKPARRV NLPPVAVVSP QLQELTLPLT SALIDGSQST DDEIVSYHW EEINGPFTEE
481 KTSVDSPLVR LSNLDPGNYS FRLTVTDSOG ATNSTTAALI VNNAVDPFPV ANAGPNBTIT
541 LPQNSITLNG NQSSDDHQIV LYEWSLGFGS EGKHVVMQGV QTPYLHLSAM QEGDYTFQLK
601 VTDSSRQQST AVVTIVVQPE NNRPPVAVAG PDKELIFPVE SATLDGSSSS DDHGIVFYHW
661 EHVRGPSAVE MENIDKAIAT VTGLQVGTYH FRLTVKDQQG LSSTSTLTVA VKKENNSPPR
721 ARAGGRHVLV LPNNSITLDG SRSTDQQRIV SYLWIRDGQS PAAGDVIDGS DHSVALQLTN
781 LVEGVYTFHL RVTDSQGASD TDTATVEVQP DPRKSGLEVEL TLQVGVGQLT EQRKDTLVRQ
841 LAVLLNVLDS DIKVQKIRAH SDLSTVIVFY VQSRPPFKVL KAAEVARNLB MRLSKEKADF
901 LLFKVLRVDT AGCLLKCSGH GHCDPLTKRC ICSHLWMENL IQRYIWDGES NCEWSIFYVT
961 VLAFTLIVLT GGFTWLCICC CKRQKRTKIR KTKYITILDN MDEQERMELR PKYGIKHRST
1021 EHNSSLMVSE SEFDSQDQTI FSREKMERGN PKVSMNGSIR NGASFYSYCSK DR

Figure 4: Expression of 254P1D6b in 293T cells

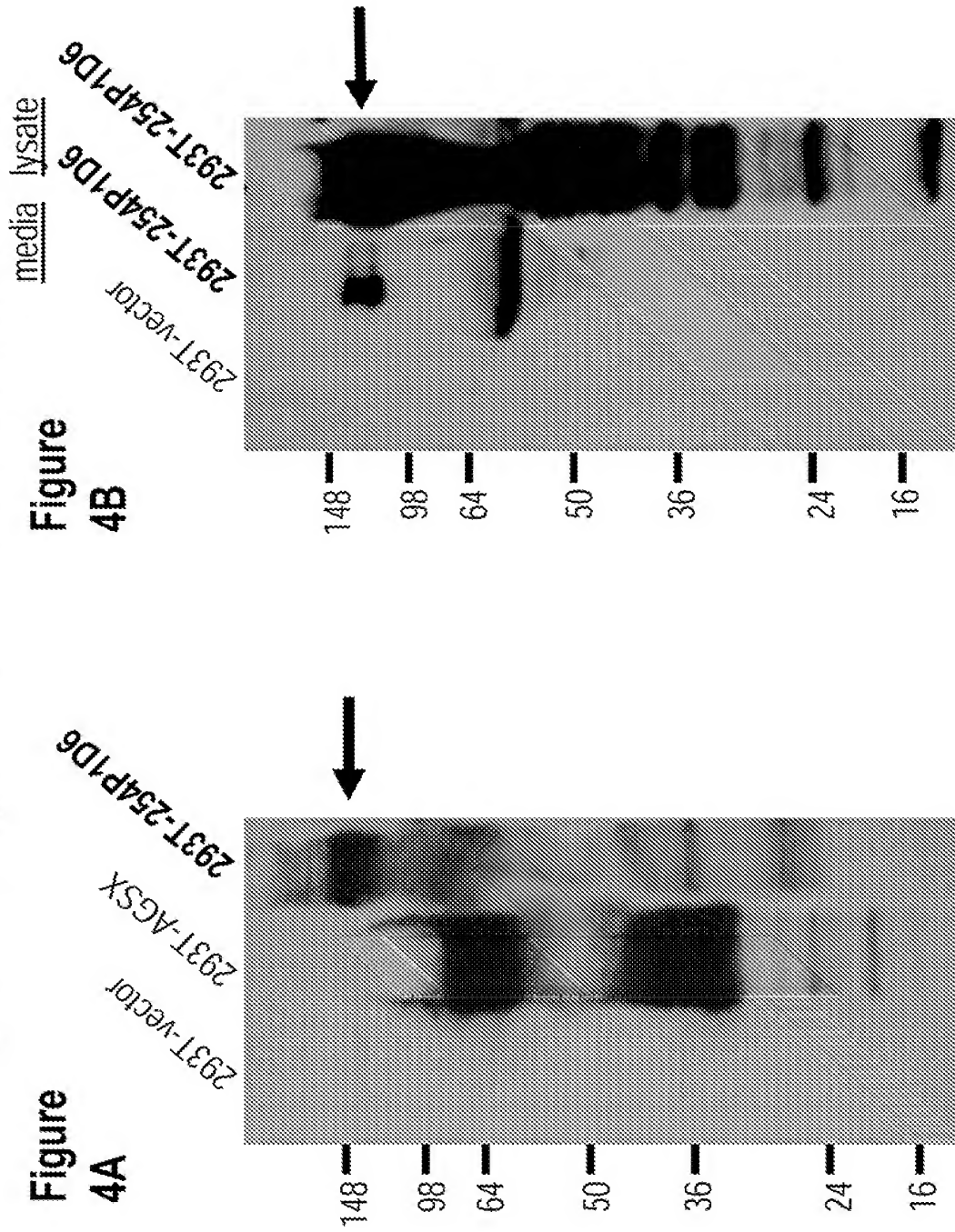


Figure 5: 254P1D6B variant 1
Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981.
Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

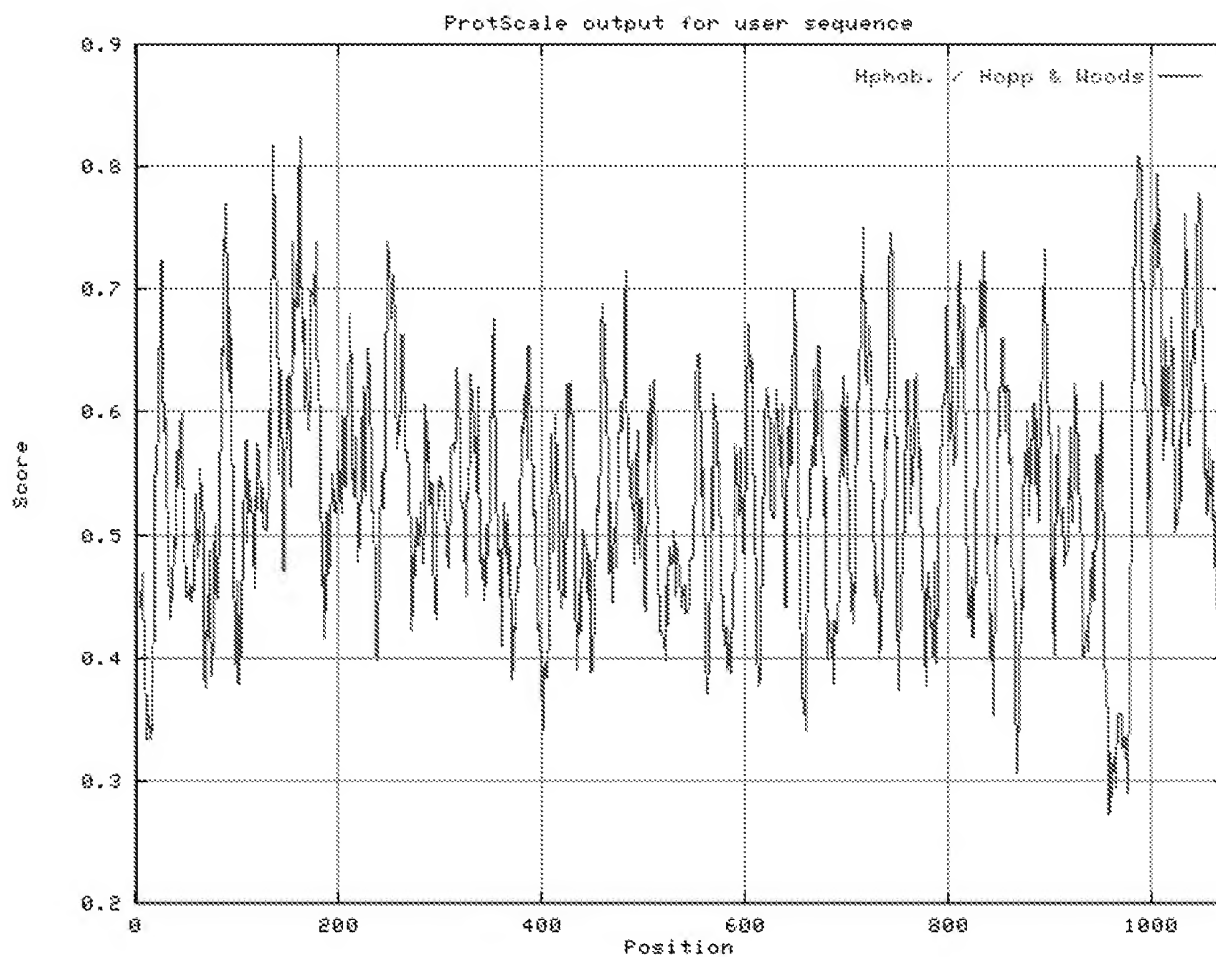


Figure 6: 254P1D6B variant 1
Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

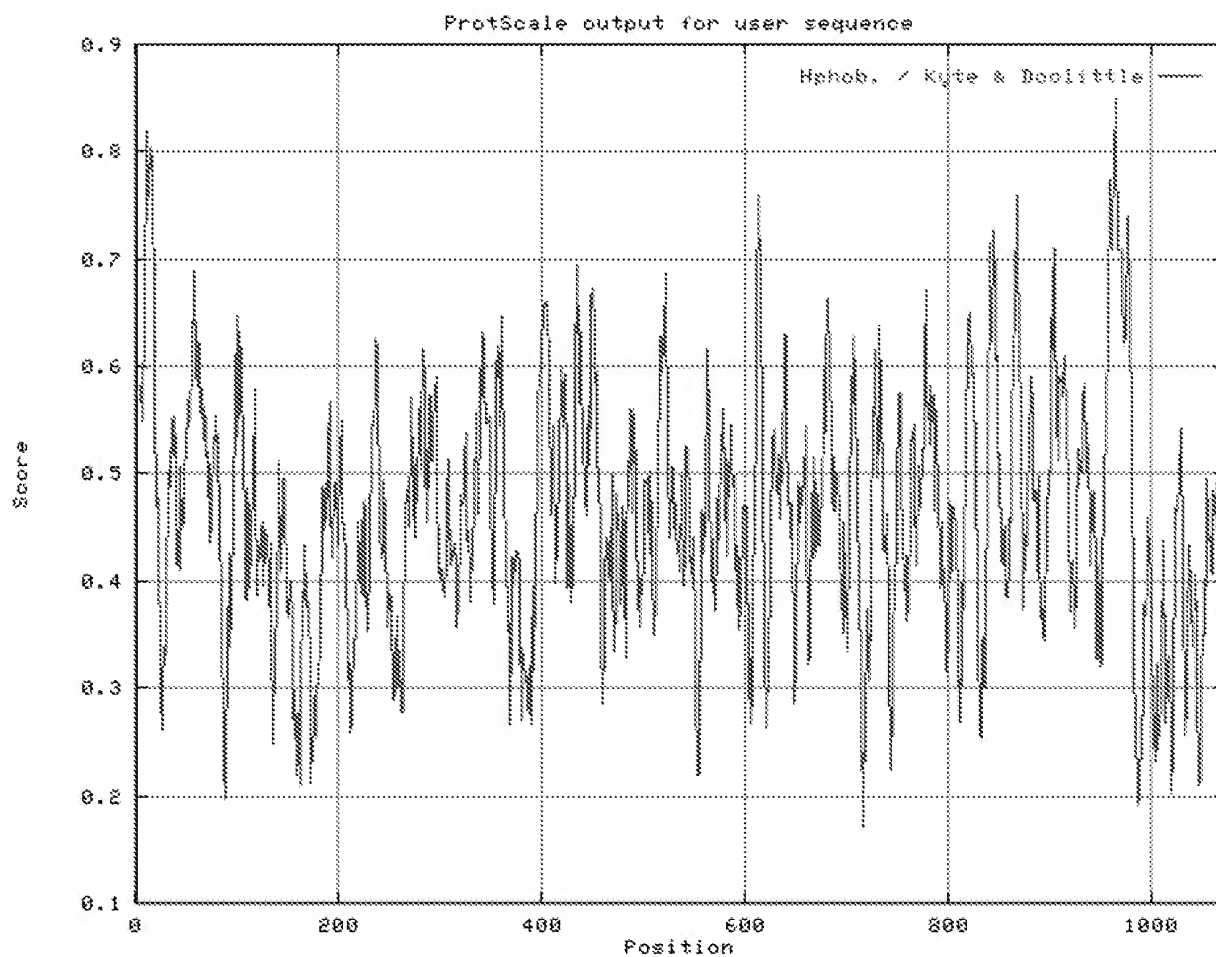


Figure 7: 254P1D6B variant 1
% Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

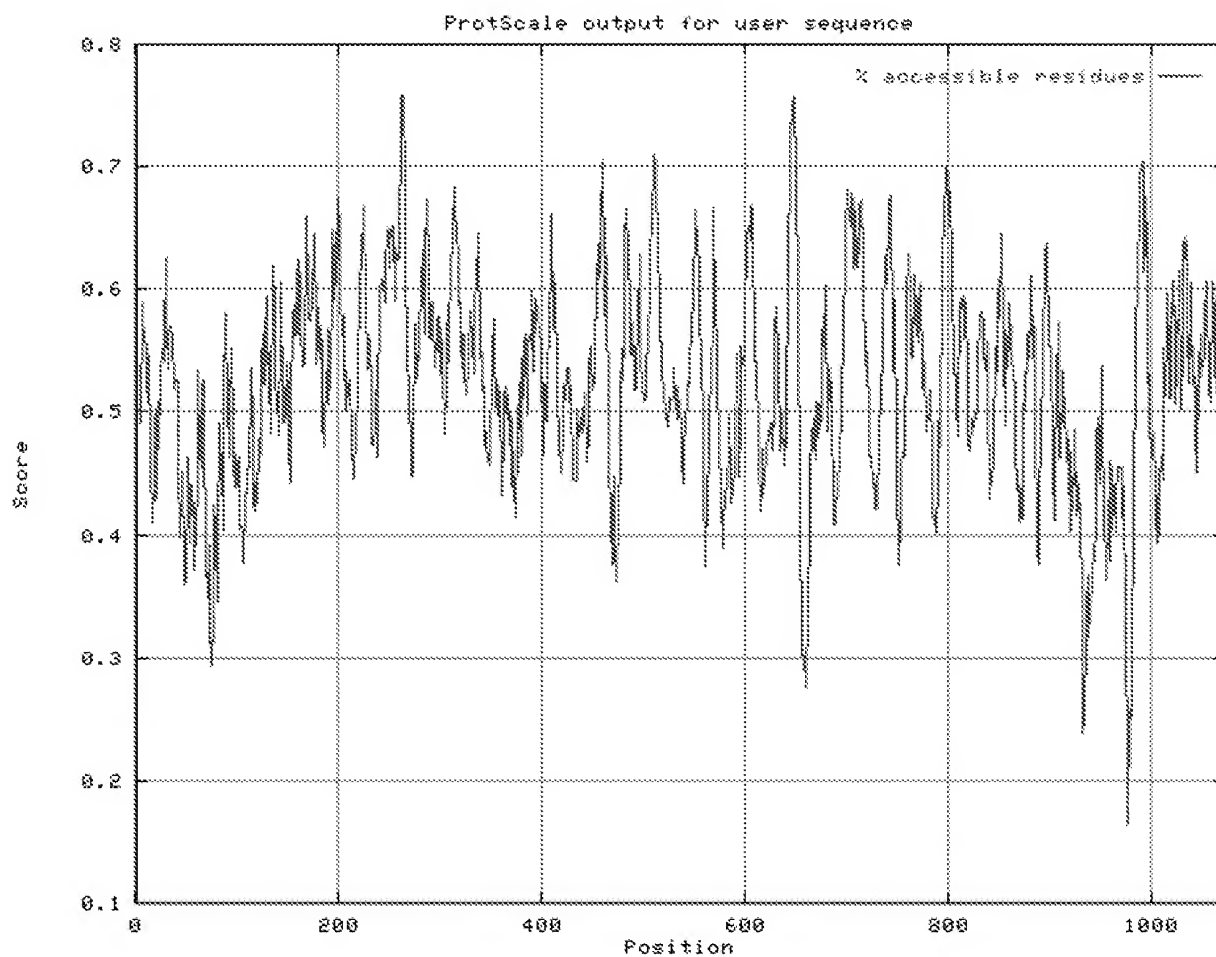


Figure 8: 254P1D6B variant 1
Average Flexibility Profile
(Bhaskaran R., Ponnuswamy P.K., 1988.
Int. J. Pept. Protein Res. 32:242-255)

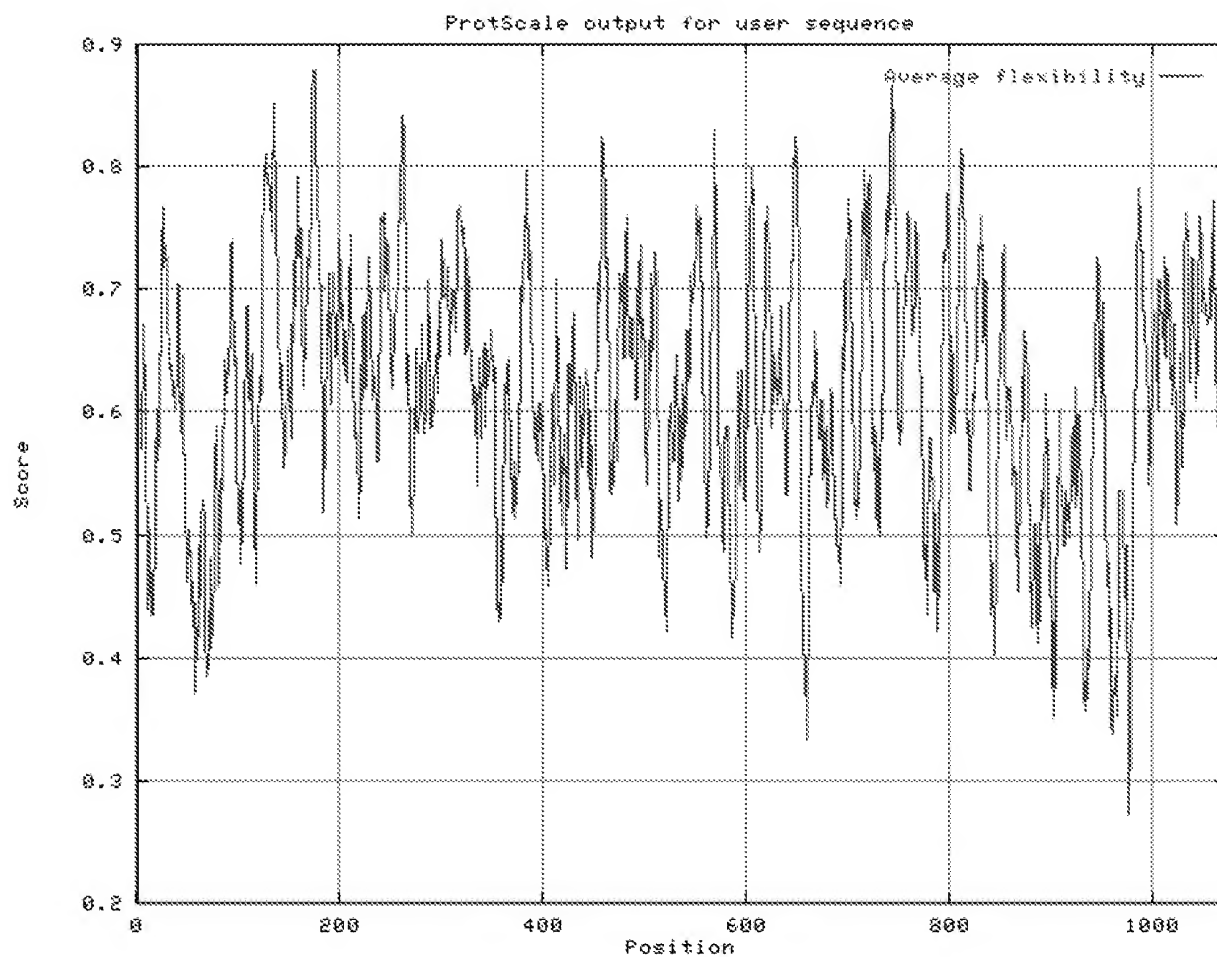


Figure 9: 254P1D6B variant 1
Beta-turn Profile
(Deleage, G., Roux B. 1987.
Protein Engineering 1:289-294)

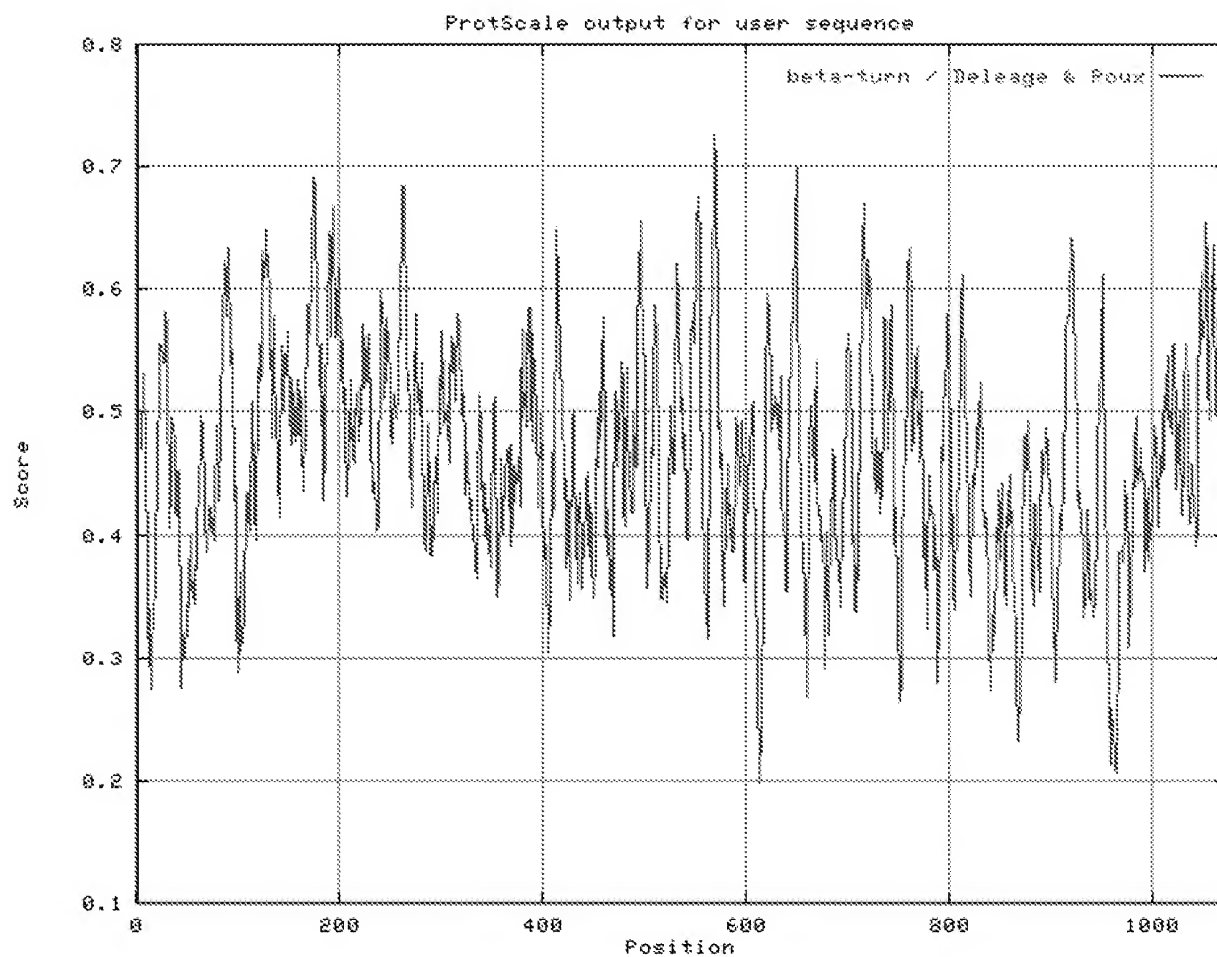


Figure 10

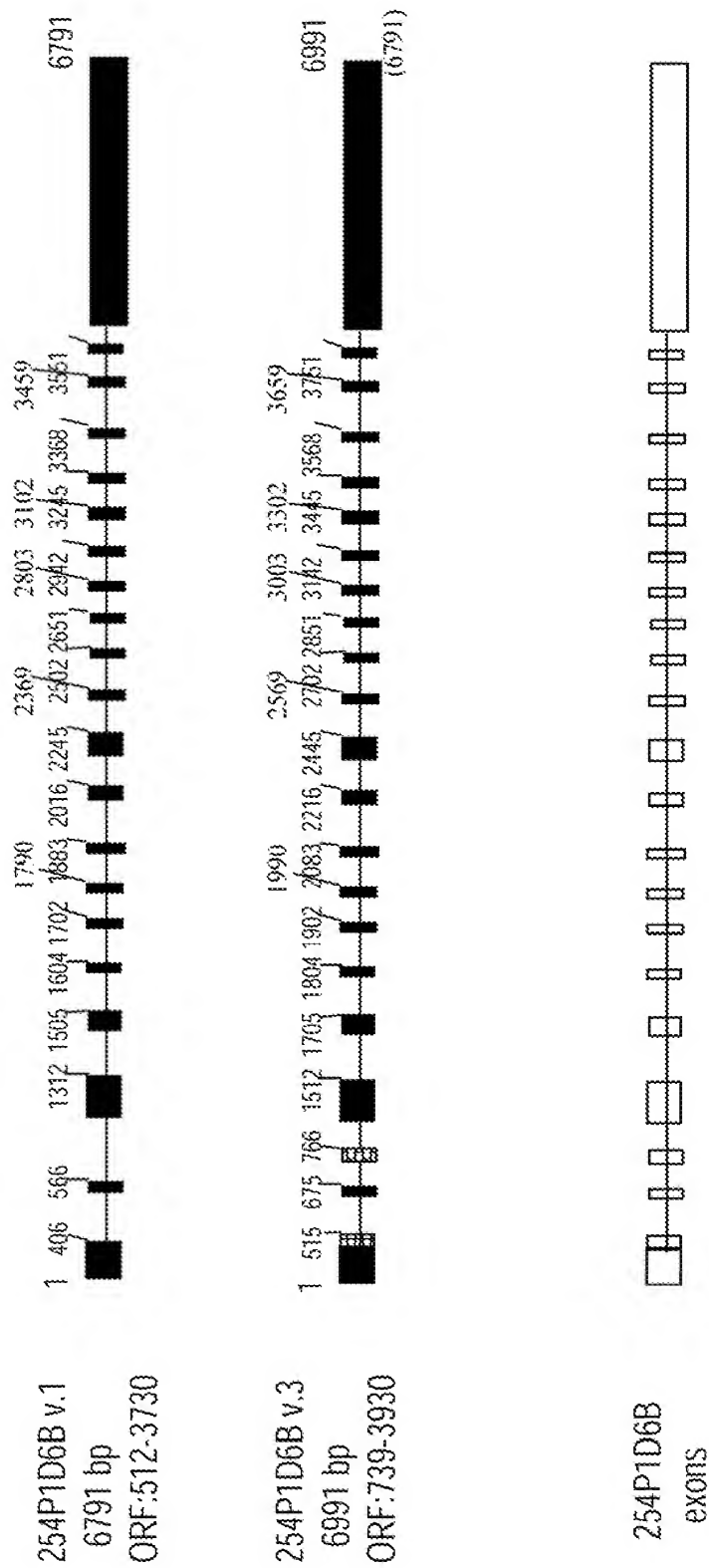


Figure 11

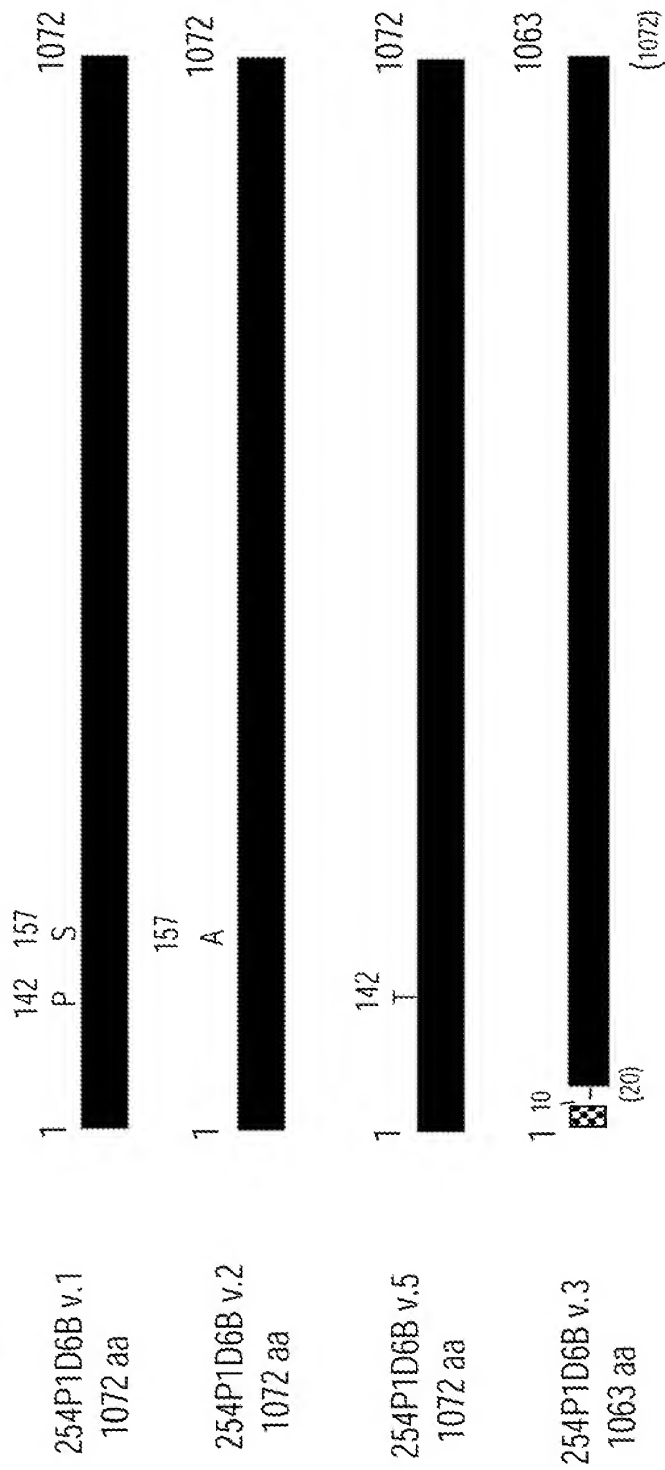


Figure 12

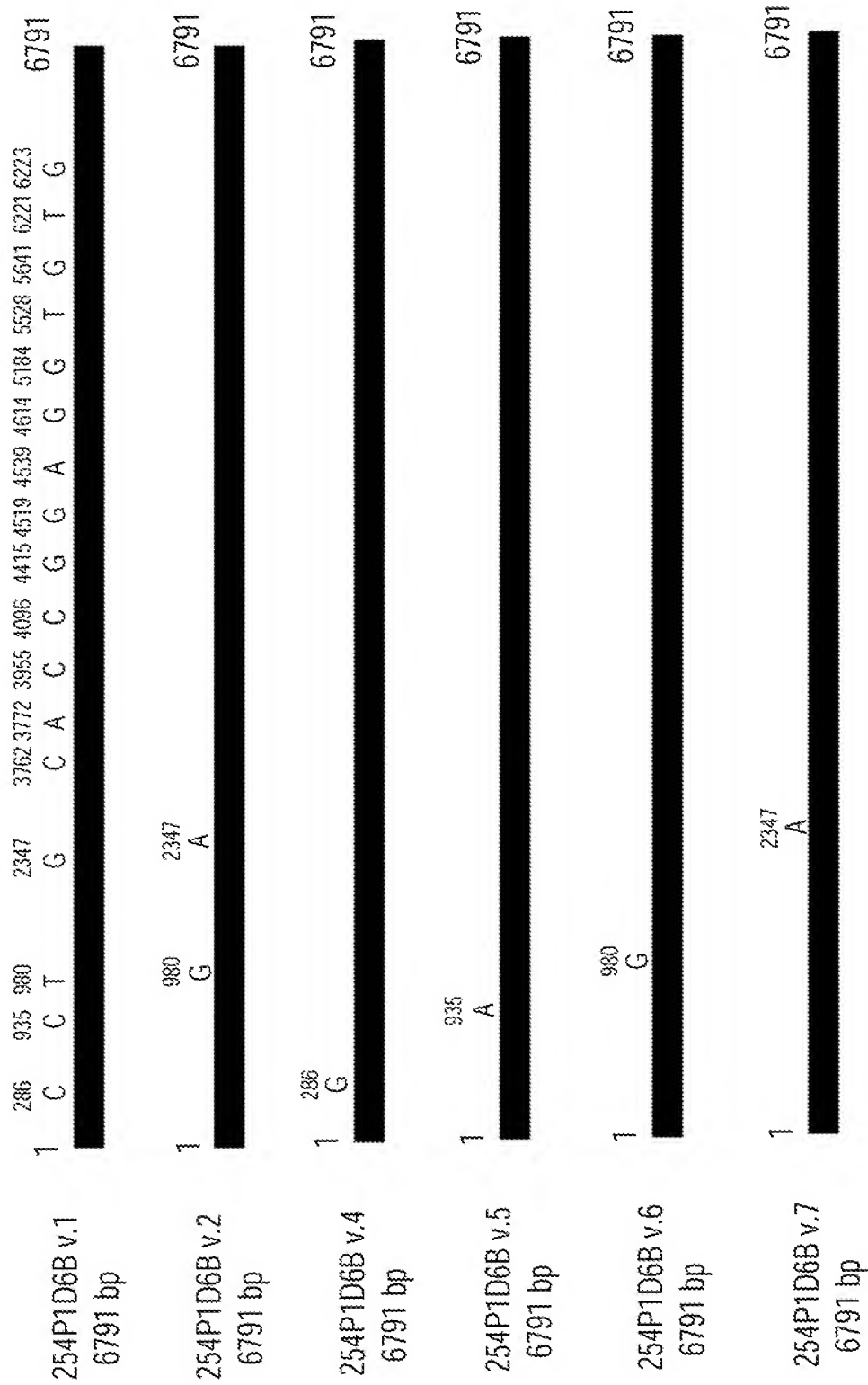


Figure 12-2

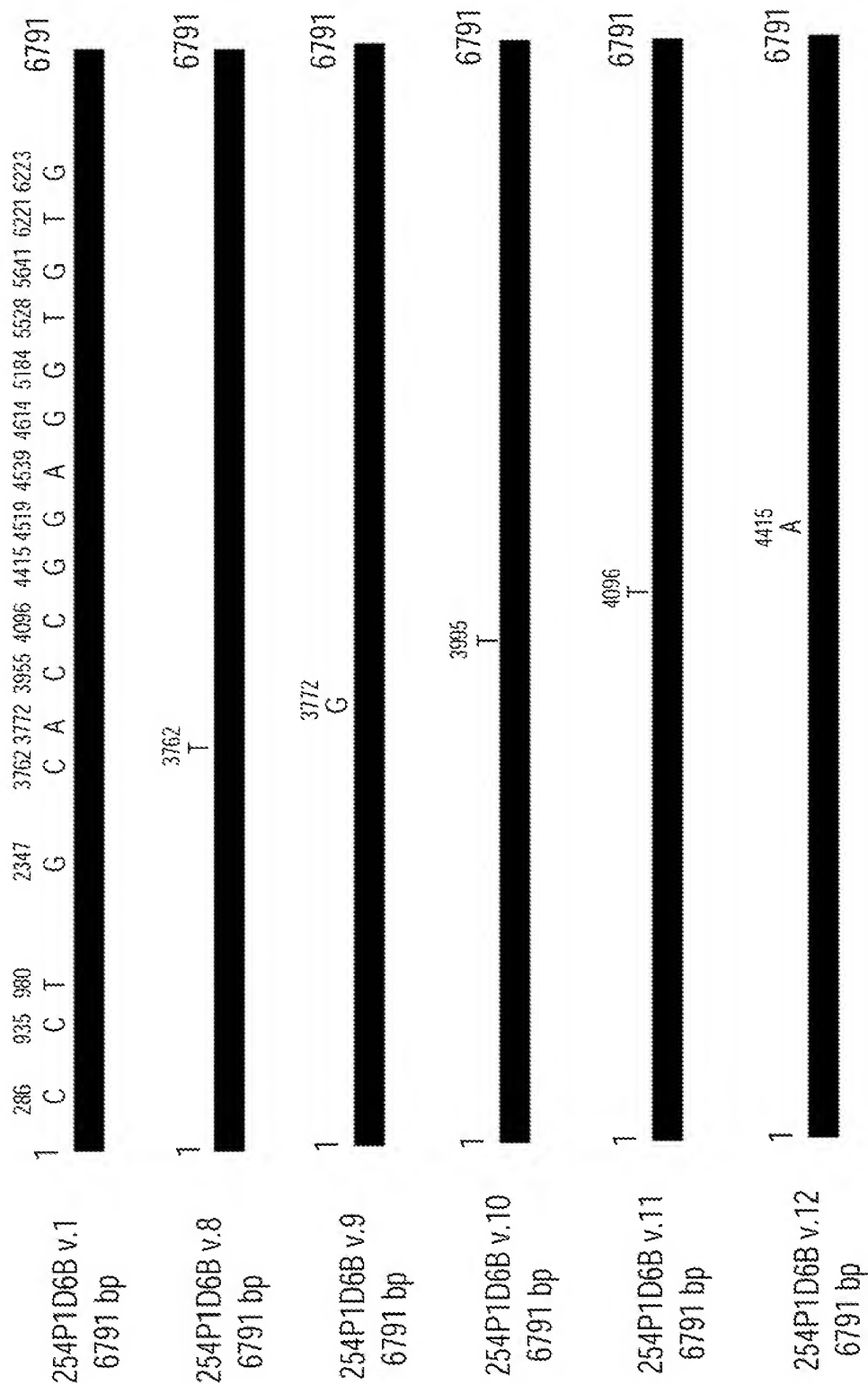


Figure 12-3

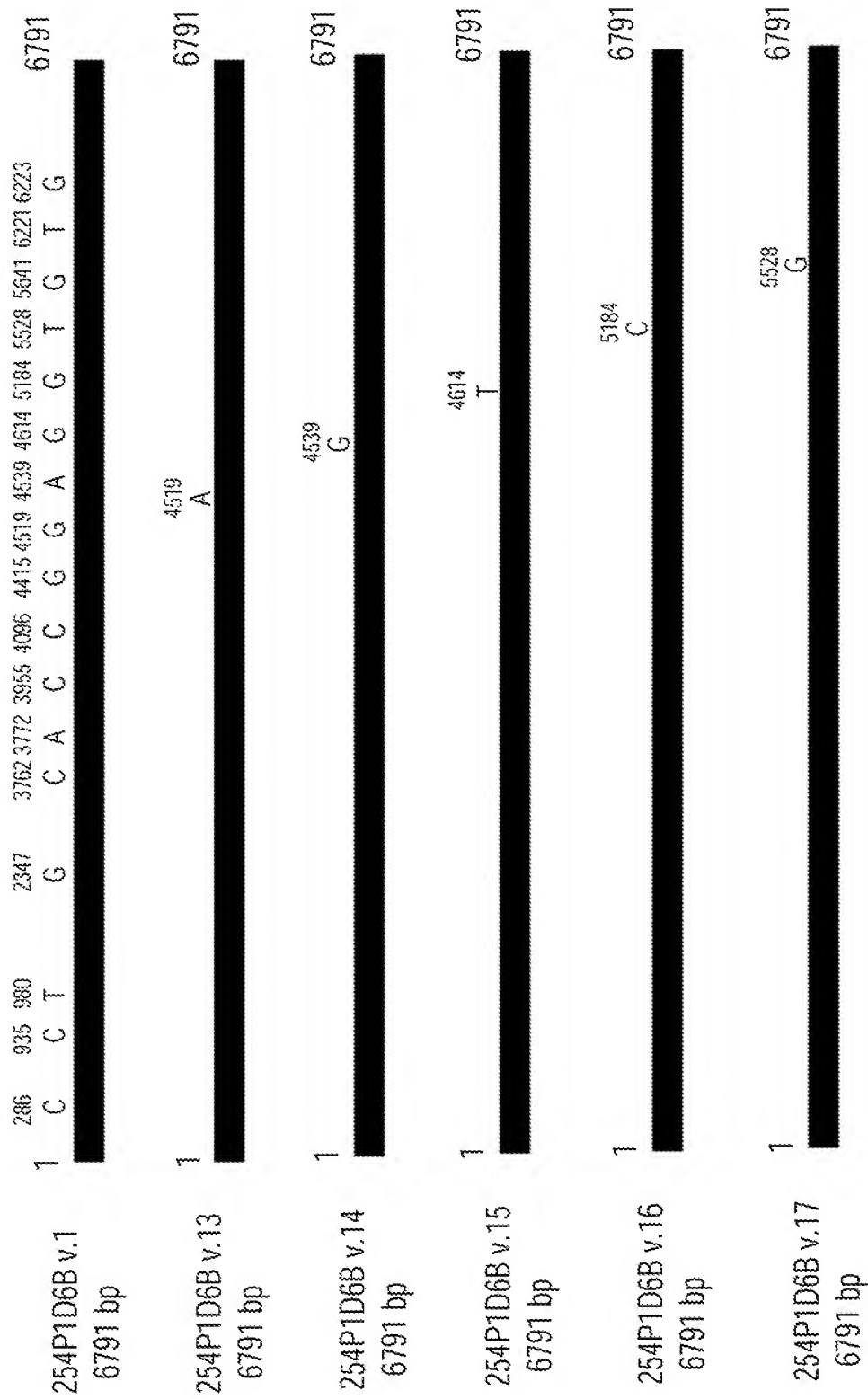


Figure 12-4

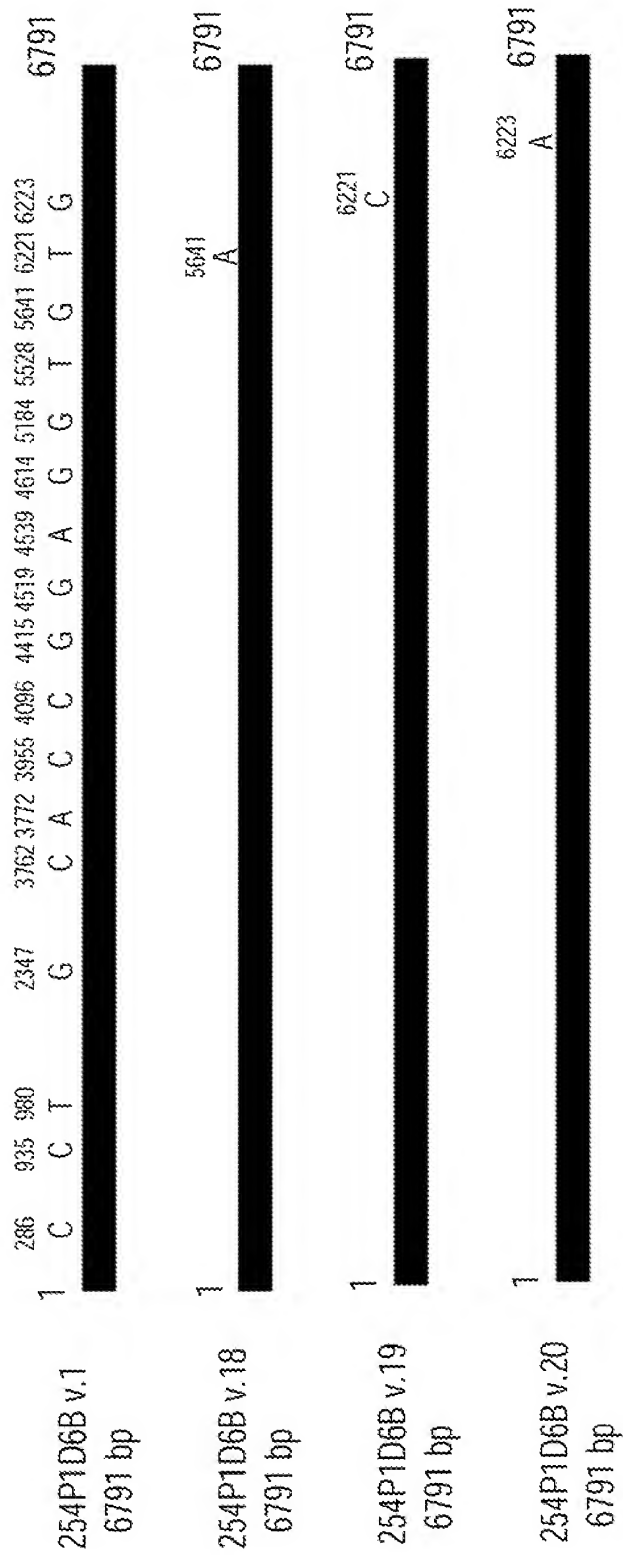


Figure 13A: Secondary structure prediction of 254P1D6B variant 1

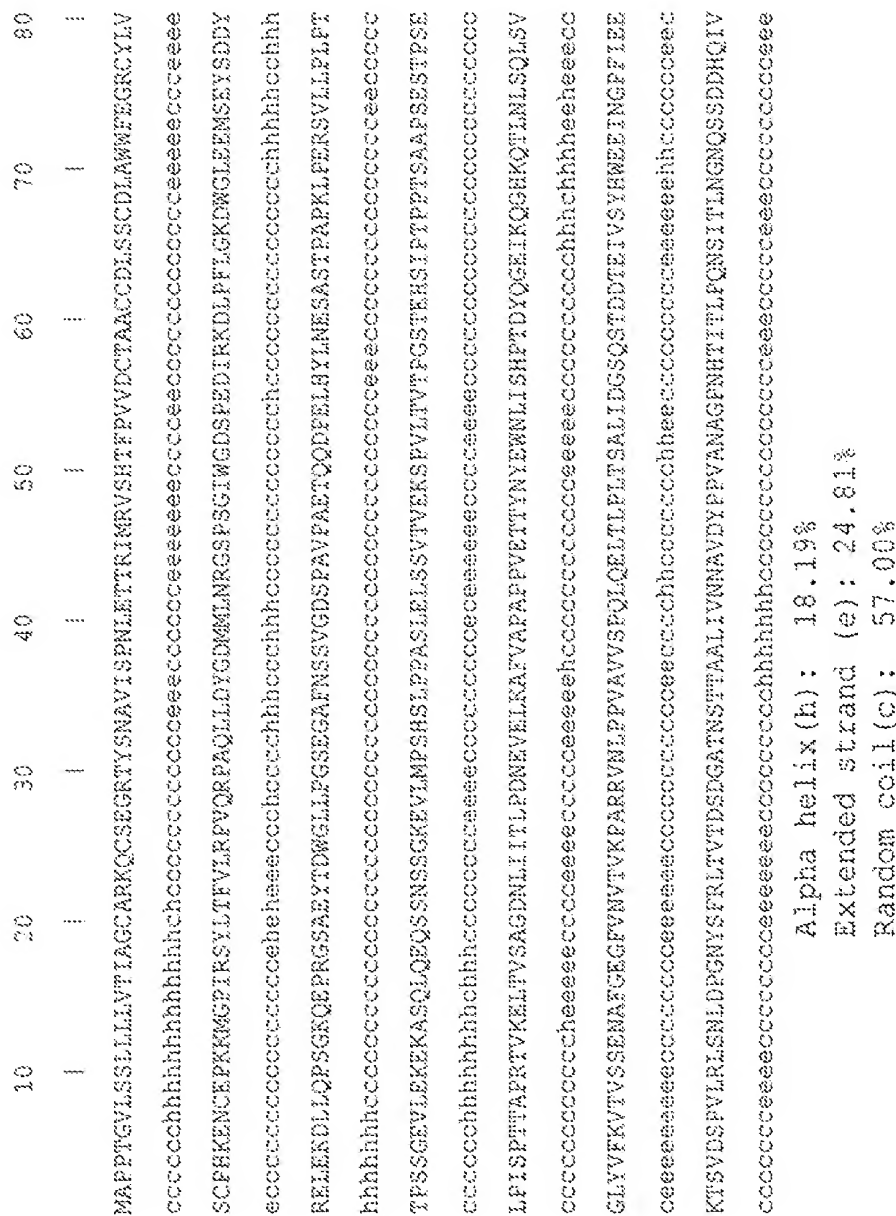
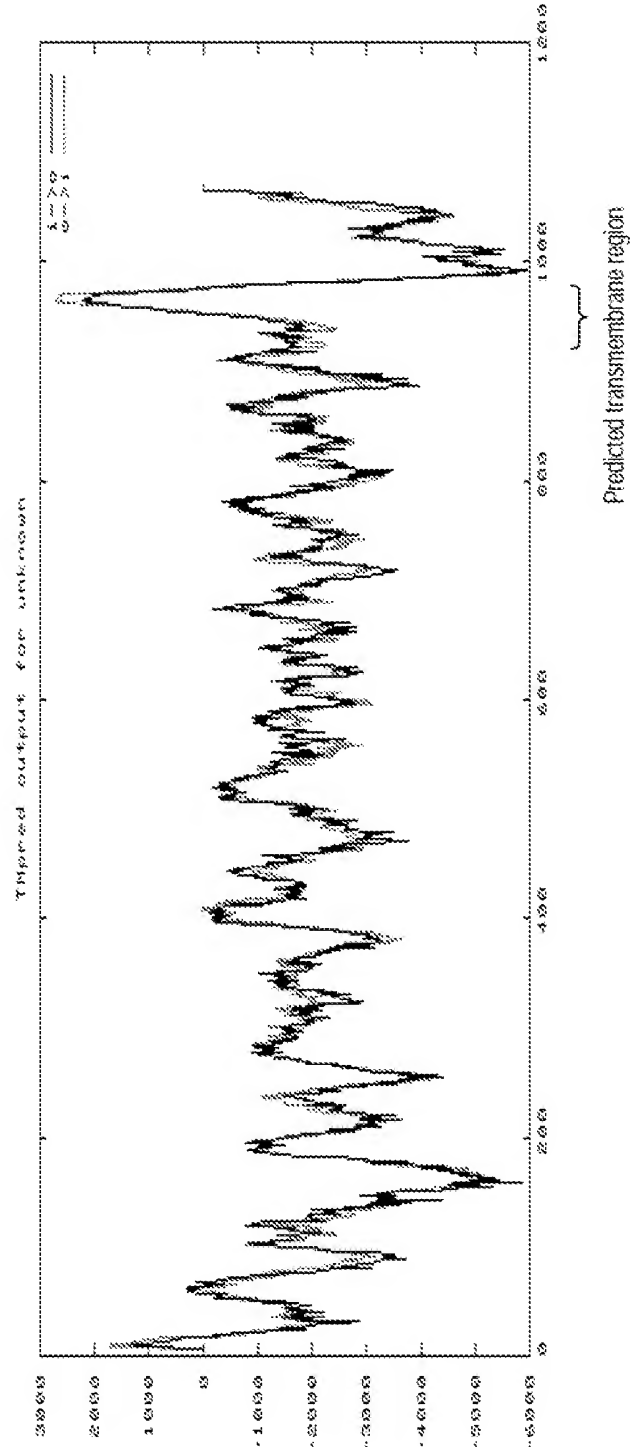


Figure 13A-2

570	580	590	600	610	620	630	640
I	I	I	I	I	I	I	I
LIENSLGPGSECKHVMQGVCTFYHLISAMQEGDITFQLKUTDSSRQQSTAVTVIVQFENNRPVAVAGFDKELIFFVE	eeeecc	SAELGSSSSDDHGIVFTHWEHVNGPSAVEMENIDKALATVTGLQVGYTHRLTVKDDQGLSSSTLTIVAVKKNNSPPR	cc	ARAGREHVLVLPNNSITLDGSRSTDDQRIVSYLINRQGSFAAGDIVDGSDBHSAIQLTNLVEGYTEHLRVTDSSQGASD	cc	TDTATVEVQDPDRKSGLVELTLQVGVGQLEKORKNDTLVPQLAVLLNVLDSDIKVKIRAHSDLTSTVIVFYVQSRPPFKVL	cc
KAAEVARNLHMRLSKEKADLLEFKVLRVDTAGCLLKCSGCHCDPLTKRCICSHLWMENLIQRYIWDGSENCENSIFYVT	hh	VLAFTLIVITGGFTWLCICCKRQKRTKIRKTKYFILDNWDQERMELRPKYGIKHSSTEHNSSLIMVSESEFDSTQDTI	hh	FSREKMERGNPKVSMNGSIRNGASFSYCSKDR	ehhh		

Alpha helix(h): 18.19%
 Extended strand (e): 24.81%
 Random coil(c): 57.00%

Figure 13B: Transmembrane prediction for 254P1D6B variant 1



1 transmembrane domain predicted

Figure 13C: Transmembrane prediction for 254P1D6B variant 1

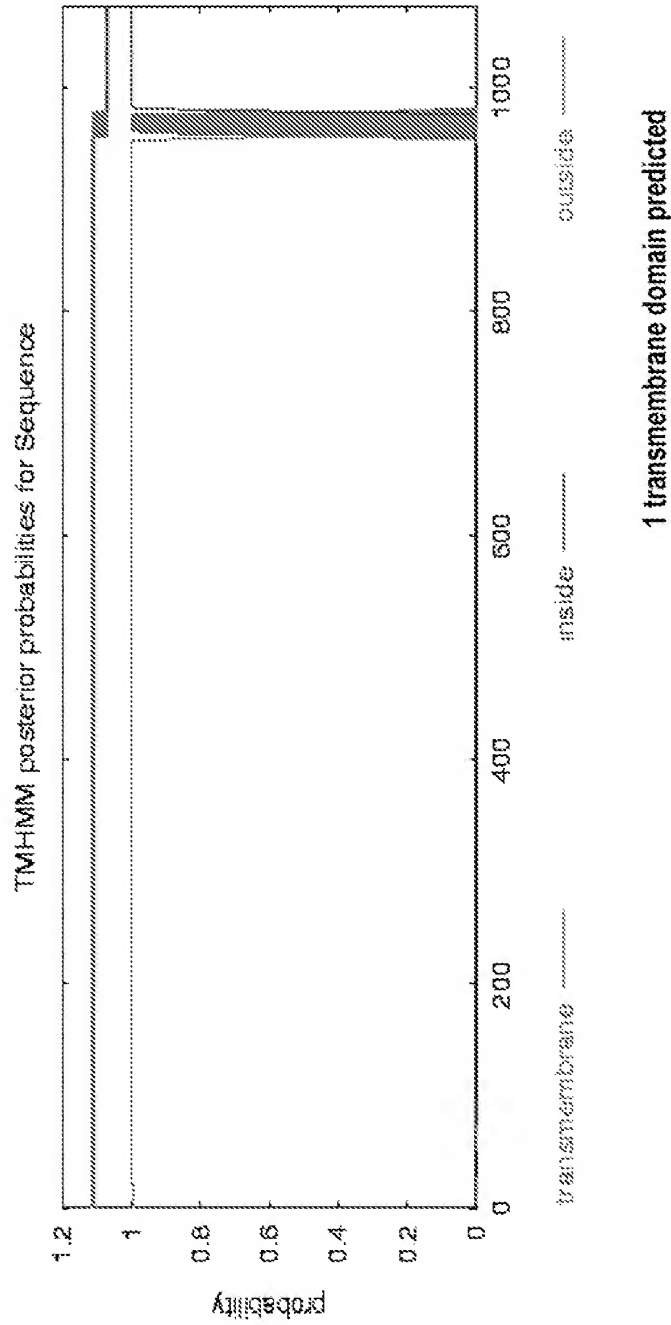


Figure 14A: 254P1D6B Expression by RT-PCR

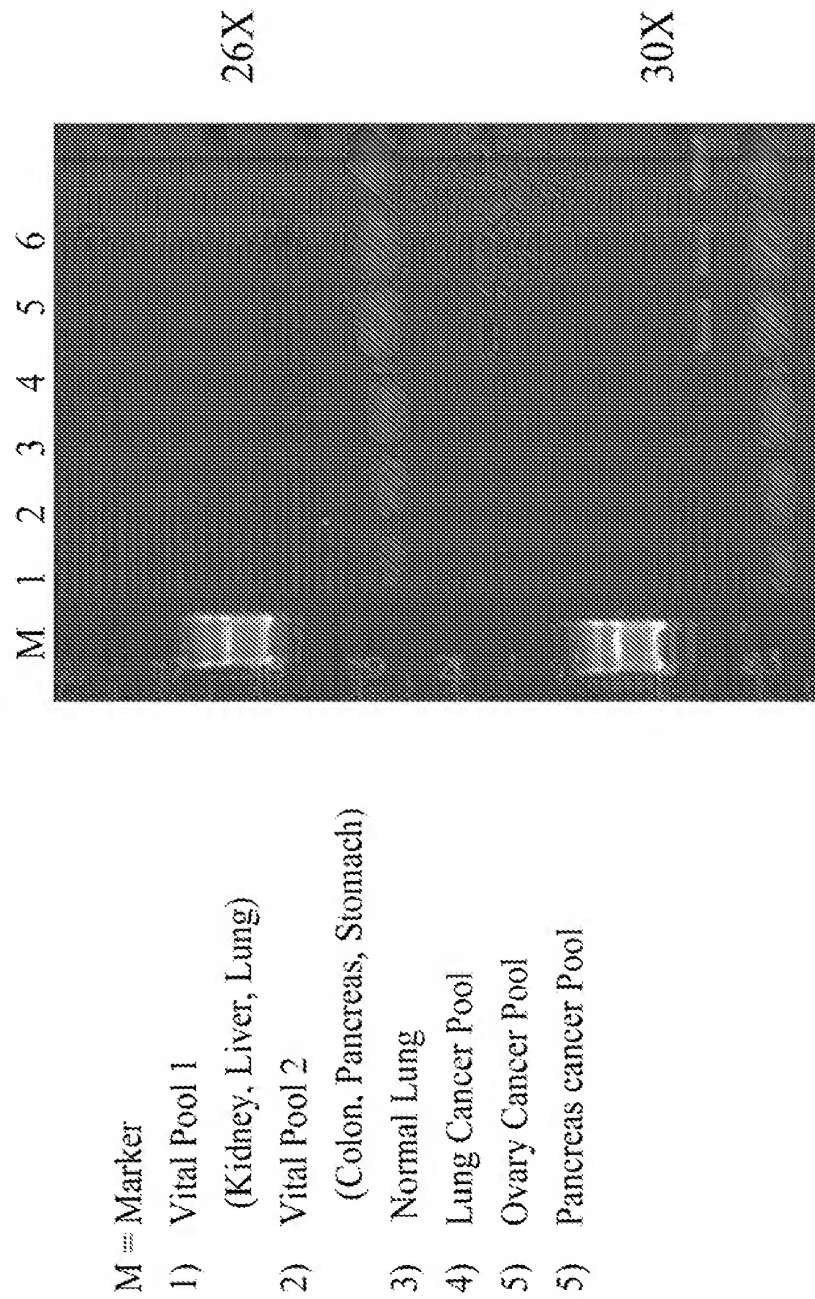


Figure 14B: Expression of 254P1D6B in Normal Human Tissues and Ovarian Cancer Patient Specimens

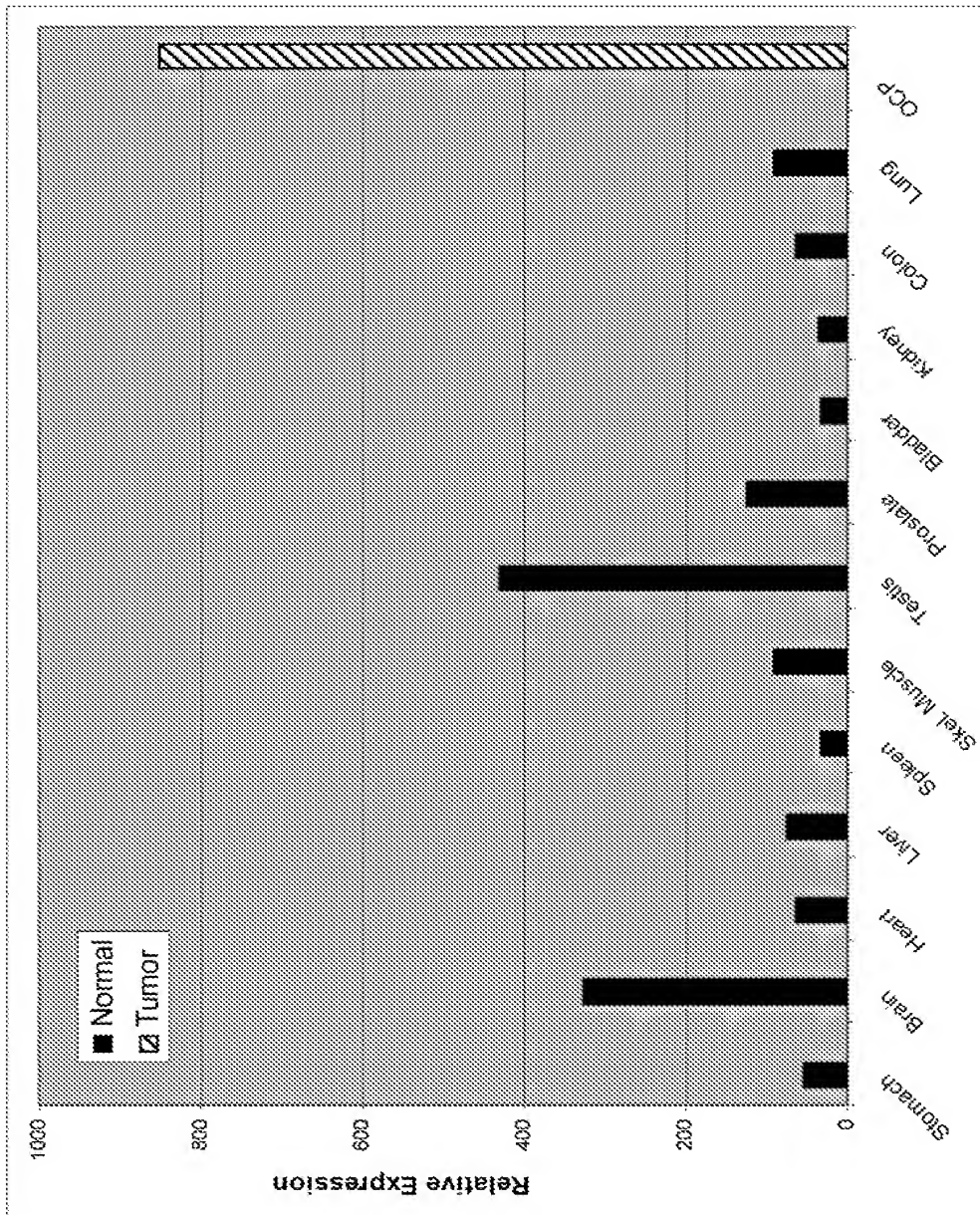


Figure 15: Expression of 254P1D6B in Normal Tissues

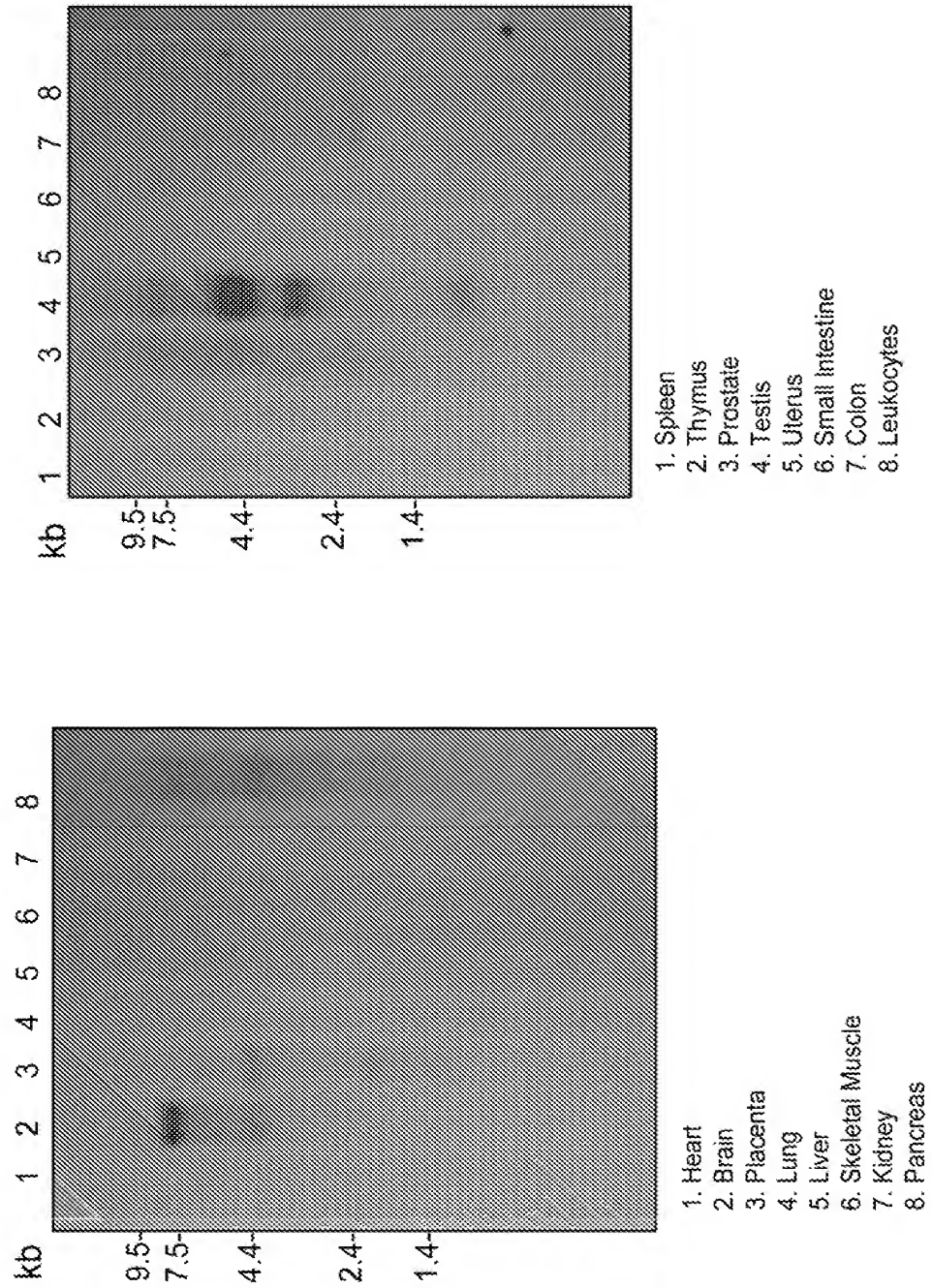


Figure 16: Expression of 254P1D6B in Lung Cancer Patient Specimens

